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301

Marvich, Maria  
Thursday, November 11, 2004 6:27 AM  
STIC-Biotech/ChemLib  
10/820133

Please search SEQ ID NO 39-43 and 1-5

each 25 nucleotides- Thank you

Maria Bonovich Marvich

United States Patent and Trademark Office

Remsen 2B84

AU 1636

Mail Box 2C70

571-272-0774

39-NA - 25  
40- | - 25  
41- | - 25  
42- | - 25  
43-NA - 25  
1-NA - 25  
2- | - 25  
3- | - 25  
4- | - 25  
5-NA - 25

mej

Mar 133  
11/15 2h

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Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

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Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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From: Marvich, Maria  
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## Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

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## Vendors and cost where applicable

STN: \_\_\_\_\_  
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4	19.6	78.4	25	6	AR124524	Sequence
5	19.6	78.4	25	6	AR124525	Sequence
6	19.6	78.4	25	6	AR163172	Sequence
7	19.6	78.4	25	6	AR163173	Sequence
8	19.6	78.4	25	6	AR163174	Sequence
9	19.6	78.4	25	6	AR163175	Sequence
10	19.6	78.4	25	6	AR163176	Sequence
11	19.6	78.4	25	6	AR493773	Sequence
12	19.6	78.4	25	6	AR493774	Sequence
13	19.6	78.4	25	6	AR493775	Sequence
14	19.6	78.4	25	6	AR493776	Sequence
15	19.6	78.4	25	6	AR493777	Sequence
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JOURNAL Patent: US 6171861-A 2 09-JAN-2001;
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          source
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Best Local Similarity 84.0%; Pred. No. 46;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

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LOCUS
DEFINITION Sequence 3 from patent US 6171861.
ACCESSION ARI124523
VERSION ARI124523.1 GI:14109884
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
PATENT: US 6171861-A 3 09-JAN-2001;
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Best Local Similarity 76.0%; Pred. No. 46;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
DEFINITION Sequence 4 from patent US 6171861.
ACCESSION ARI124524
VERSION ARI124524.1 GI:14109885
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
PATENT: US 6171861-A 4 09-JAN-2001;
FEATURES Location/Qualifiers
          source
ORIGIN
Query Match 78.4%; Score 19.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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JOURNAL Patent: US 6171861-A 2 09-JAN-2001;
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Best Local Similarity 84.0%; Pred. No. 46;
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LOCUS
DEFINITION Sequence 5 from patent US 6171861.
ACCESSION ARI124525
VERSION ARI124525.1 GI:14109886
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
PATENT: US 6171861-A 5 09-JAN-2001;
FEATURES Location/Qualifiers
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Db 1 GTTCAGCTTYYKTRTACNAACTSGB 25

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DEFINITION Sequence 1 from patent US 6270969.
ACCESSION ARI163172
VERSION ARI163172.1 GI:16233677
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
PATENT: US 6270969-A 1 07-AUG-2001;
FEATURES Location/Qualifiers
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DEFINITION Sequence 2 from patent US 6270969.
ACCESSION ARI163173
VERSION ARI163173.1 GI:16233679
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
PATENT: US 6270969-A 2 07-AUG-2001;
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Db 1 AGCCWGCTTTTKRTACNAAGTSG 25

RESULT 8  
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LOCUS AR163174 25 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 3 from patent US 6270969.  
ACCESSION AR163174  
VERSION AR163174.1 GI:16233681  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: US 6270969-A 3 07-AUG-2001;  
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Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTCKRTACNAAGTSG 25

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DEFINITION Sequence 4 from patent US 6270969.  
ACCESSION AR163175  
VERSION AR163175.1 GI:16233683  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: US 6270969-A 4 07-AUG-2001;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 78.4%; Score 19.6; DB 6; Length 25;  
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Db 1 AGCCWGCTTTCKRTACNAAGTSG 25

RESULT 10  
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LOCUS AR163176 25 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 5 from patent US 6270969.  
ACCESSION AR163176  
VERSION AR163176.1 GI:16233684  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: US 6270969-A 5 07-AUG-2001;  
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Db 1 GTTCAGCTTTTKRTACNAAGTSG 25

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LOCUS AR493773 25 bp mRNA linear PAT 15-MAY-2004  
DEFINITION Sequence 1 from patent US 6720140.  
ACCESSION AR493773  
VERSION AR493773.1 GI:47266182  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: US 6720140-A 1 13-APR-2004;  
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Query Match 78.4%; Score 19.6; DB 6; Length 25;  
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Db 1 RKYCWGCTTTTKRTACNAASTSG 25

RESULT 12  
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LOCUS AR493774 25 bp mRNA linear PAT 15-MAY-2004  
DEFINITION Sequence 2 from patent US 6720140.  
ACCESSION AR493774  
VERSION AR493774.1 GI:47266184  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: US 6720140-A 2 13-APR-2004;  
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Db 1 AGCCWGCTTYYKTRTACNAAGTSG 25

RESULT 13
LOCUS AR493775 25 bp mRNA linear PAT 15-MAY-2004
DEFINITION Sequence 3 from patent US 6720140.
ACCESSION AR493775
VERSION AR493775.1 GI:47266186
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 3 13-APR-2004;
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Query Match 78.4%; Score 19.6; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 46;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 4 from patent US 6720140.
ACCESSION AR493776
VERSION AR493776.1 GI:47266188
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 4 13-APR-2004;
FEATURES
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Db 1 AGCCWGCTTYYKTRTACNAAGTSG 25

RESULT 15
LOCUS AR493777 25 bp mRNA linear PAT 15-MAY-2004
DEFINITION Sequence 5 from patent US 6720140.
ACCESSION AR493777
VERSION AR493777.1 GI:47266190
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 5 13-APR-2004;
FEATURES
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Best Local Similarity 80.0%; Pred. No. 46;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Job time : 709.5 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds  
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Title: US-10-820-133-1

Perfect score: 25

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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12: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	19.6	78.4	25	2 AAT48210	Aat48210 M-att cor
3	19.6	78.4	25	2 AAT48213	Aat48213 M-attL co
4	19.6	78.4	25	2 AAT48214	Aat48214 M-attPl c
5	19.6	78.4	25	2 AAT48211	Aat48211 M-attB co
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11	19.6	78.4	25	2 AAX78937	Aax78937 Oligonucl
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13	19.6	78.4	25	2 AAX78939	Aax78939 Oligonucl
14	19.6	78.4	25	4 AAS06185	Aas06185 Phase-lam
15	19.6	78.4	25	4 AAC87867	Aac87867 Escherich
16	19.6	78.4	25	4 AAC87868	Aac87868 Escherich
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20	19.6	78.4	25	4 AAF55736	Aaf55736 Recombina
21	19.6	78.4	25	4 AAF55738	Aaf55738 Recombina

#### ALIGNMENTS

##### RESULT 1

AAT48212  
ID AAT48212 standard; DNA; 25 BP.

XX AAT48212;

XX AC

XX 20-OCT-1997 (first entry)

XX DT

XX DE M-attr core region.

XX XX

XX att recombination site; core region; mutation; enhance; recombination;

XX KW vector; subcloning; regulation; exchange; ss.

XX OS Synthetic.

XX XX

XX WO9640724-A1.

XX FN

XX PD

XX 19-DEC-1996.

XX XX

XX PF 07-JUN-1996; 96WO-US010082.

XX XX

XX PR 07-JUN-1995; 95US-00486139.

XX XX

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX PA

XX XX

XX PI Hartley JL, Brasch MA;

XX XX

XX WPI; 1997-065168/06.

XX XX

XX PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -

XX PT using recombinant proteins and engineered recombination sites in vitro or

XX PT in vivo.

XX XX

XX PS Claim 14; Page 55; 106pp; English.

XX XX

XX CC AAT48210-25 are att recombination site core region DNA sequences. The

XX CC core region has at least one engineered mutation that enhances

XX CC recombination in vitro in the formation of a Cointegrate or Product DNA.

XX CC These core regions can be incorporated into novel vector donor DNA

XX CC molecules. The nucleic acids, vectors and methods of the invention are

XX CC used to obtain chimeric nucleic acid using recombination proteins and

XX CC engineered recombination sites in vitro or in vivo. The improved

XX CC specificity, speed and yields of the invention facilitates DNA or RNA

XX CC subcloning, regulation or exchange useful for any related purpose, e.g.

XX CC

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

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 Best Local Similarity 76.0%; Pred. No. 12;  
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 Db 1 GTTCAGCTTTCCKTRTACNAASTSGB 25

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XX AC AAT48210;

XX DT 20-OCT-1997 (first entry)

XX DE M-att core region.

XX att recombination site; core region; mutation; enhance; recombination;  
 KW vector; subcloning; regulation; exchange; ss.

XX OS Synthetic.

XX PN WO9640724-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;

XX DR WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
 PT using recombinant proteins and engineered recombination sites in vitro or  
 PT in vivo.

XX PS Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The  
 CC core region has at least one engineered mutation that enhances  
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.  
 CC These core regions can be incorporated into novel vector donor DNA  
 CC molecules. The nucleic acids, vectors and methods of the invention are  
 CC used to obtain chimeric nucleic acid using recombination proteins and  
 CC engineered recombination sites in vitro or in vivo. The improved  
 CC specificity, speed and yields of the invention facilitates DNA or RNA  
 CC subcloning, regulation or exchange useful for any related purpose, e.g.  
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA

SQ Sequence 25 BP; 3 A; 3 C; 2 G; 6 T; 0 U; 11 Other;

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ID AAT48213 standard; DNA; 25 BP.

XX AC AAT48213;

XX DT 20-OCT-1997 (first entry)

XX DE M-attL core region.

XX att recombination site; core region; mutation; enhance; recombination;  
 KW vector; subcloning; regulation; exchange; ss.

XX OS Synthetic.

XX PN WO9640724-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;

XX DR WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
 PT using recombinant proteins and engineered recombination sites in vitro or  
 PT in vivo.

XX PS Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The  
 CC core region has at least one engineered mutation that enhances  
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.  
 CC These core regions can be incorporated into novel vector donor DNA  
 CC molecules. The nucleic acids, vectors and methods of the invention are  
 CC used to obtain chimeric nucleic acid using recombination proteins and  
 CC engineered recombination sites in vitro or in vivo. The improved  
 CC specificity, speed and yields of the invention facilitates DNA or RNA  
 CC subcloning, regulation or exchange useful for any related purpose, e.g.  
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA

SQ Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 12;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25

Db 1 AGCCWGCCTTTCCKTRTACNAAGTSGB 25

RESULT 4

AAT48214

ID AAT48214 standard; DNA; 25 BP.

XX AC AAT48214;

XX DT 20-OCT-1997 (first entry)

XX DE M-attP1 core region.

XX att recombination site; core region; mutation; enhance; recombination;  
 KW vector; subcloning; regulation; exchange; ss.

XX

OS Synthetic.  
 XX WO9640724-A1.  
 PN 19-DEC-1996.  
 XX 07-JUN-1996; 96WO-US010082.  
 XX 07-JUN-1995; 95US-00486139.  
 XX (LIFE-) LIFE TECHNOLOGIES INC.  
 XX Hartley JL, Brasch MA;  
 PI  
 XX WPI; 1997-065168/06.  
 DR Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
 XX using recombinant proteins and engineered recombination sites in vitro or  
 PT in vivo.  
 XX Claim 14; Page 55; 106pp; English.  
 XX AAT48210-25 are att recombination site core region DNA sequences. The  
 CC core region has at least one engineered mutation that enhances  
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.  
 CC These core regions can be incorporated into novel vector donor DNA  
 CC molecules. The nucleic acids, vectors and methods of the invention are  
 CC used to obtain chimeric nucleic acid using recombination proteins and  
 CC engineered recombination sites in vitro or in vivo. The improved  
 CC specificity, speed and yields of the invention facilitates DNA or RNA  
 CC subcloning, regulation or exchange useful for any related purpose, e.g.  
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA  
 XX  
 SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;  
 Query Match 78.4%; Score 19.6; DB 2; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 12;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RKYCWGCTTYYKTRTACNAAGTSGB 25  
 Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25  
 RESULT 5  
 AAT48211  
 ID AAT48211 standard; DNA; 25 BP.  
 XX  
 AC AAT48211;  
 XX 20-OCT-1997 (first entry)  
 DT  
 XX M-attB core region.  
 DE  
 XX att recombination site; core region; mutation; enhance; recombination;  
 KW vector; subcloning; regulation; exchange; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9640724-A1.  
 PN 19-DEC-1996.  
 XX 07-JUN-1996; 96WO-US010082.  
 XX 07-JUN-1995; 95US-00486139.  
 XX (LIFE-) LIFE TECHNOLOGIES INC.  
 XX Hartley JL, Brasch MA;  
 PI  
 XX WPI; 1997-065168/06.  
 DR Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
 XX using recombinant proteins and engineered recombination sites in vitro or  
 PT in vivo.  
 XX Claim 14; Page 55; 106pp; English.  
 XX AAT48210-25 are att recombination site core region DNA sequences. The  
 CC core region has at least one engineered mutation that enhances  
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.  
 CC These core regions can be incorporated into novel vector donor DNA  
 CC molecules. The nucleic acids, vectors and methods of the invention are  
 CC used to obtain chimeric nucleic acid using recombination proteins and  
 CC engineered recombination sites in vitro or in vivo. The improved  
 CC specificity, speed and yields of the invention facilitates DNA or RNA  
 CC subcloning, regulation or exchange useful for any related purpose, e.g.  
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA  
 XX  
 SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;  
 Query Match 78.4%; Score 19.6; DB 2; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 12;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RKYCWGCTTYYKTRTACNAAGTSGB 25  
 Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25  
 RESULT 6  
 AAX78938  
 ID AAX78938 standard; DNA; 25 BP.  
 XX  
 AC AAX78938;  
 XX 17-AUG-1999 (first entry)  
 DT  
 XX Oligonucleotide #4 for recombination and cloning method.  
 DE  
 XX Cloning; donor; recombination site; vector; chimeric; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9921977-A1.  
 PN 06-MAY-1999.  
 PD  
 XX 26-OCT-1998; 98WO-US022589.  
 XX 24-OCT-1997; 97US-0065930P.  
 PR 23-OCT-1998; 98US-00177387.  
 PR  
 XX (LIFE-) LIFE TECHNOLOGIES INC.  
 PA  
 XX Hartley JL, Brasch MA, Temple GF, Fox DK;  
 PI  
 XX WPI; 1999-303011/25.  
 DR  
 XX New nucleic acid cloning methods.  
 PT  
 XX Disclosure; Page 159; 185pp; English.  
 PS  
 XX The invention relates to novel methods for cloning or subcloning one or  
 CC more nucleic acid molecules (NAME) comprising: (a) combining in vitro or  
 CC in vivo: (i) at least one insert donor molecules (IDMs) comprising one or  
 CC more desired nucleic acid segments flanked by at least 2 recombination  
 CC sites which do not recombine with each other; (2) one or more vector  
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
 CC not recombine with each other; and (3) one or more site-specific  
 CC recombination proteins; (b) incubating the combination to transfer one or

CC more of the desired segments into one or more of the VDMs, thereby  
 CC producing one or more desired product molecules (PMs). The methods can be  
 CC used for the efficient and specific recombination of NAM segments. They  
 CC can be used to generate chimeric DNA or RNA molecules that have the  
 CC desired characteristics and/or nucleic acid segments. The methods can  
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
 CC are used in the method of the invention

SQ Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 12;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCGCTTYYKTRTACNAASTSG 25

Db 1 AGCCWGCTTCTKTRTACNAAGTSG 25

RESULT 7

AAX78945

ID AAX78945 standard; DNA; 25 BP.

XX

AC AAX78945;

XX

DT 17-AUG-1999 (first entry)

XX

DE Oligonucleotide #11 for recombination and cloning method.

XX

KW Cloning; donor; recombination site; vector; chimeric; ss.

XX

OS Synthetic.

XX

PN WO9921977-A1.

XX

PD 06-MAY-1999.

XX

PF 26-OCT-1998; 98WO-US022589.

XX

PR 24-OCT-1997; 97US-0065930P.

XX

PR 23-OCT-1998; 98US-00177387.

XX

PA (LIFE-) LIFE TECHNOLOGIES INC.

XX

PI Hartley JL, Brasch MA, Temple GF, Fox DK;

XX

DR WPI; 1999-303011/25.

XX

PT New nucleic acid cloning methods.

XX

PS Disclosure; Page 161; 185pp; English.

XX

CC The invention relates to novel methods for cloning or subcloning one or  
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
 CC more desired nucleic acid segments flanked by at least 2 recombination  
 CC sites which do not recombine with each other; (2) one or more vector  
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
 CC not recombine with each other; and (3) one or more site-specific  
 CC recombination proteins; (b) incubating the combination to transfer one or  
 CC more of the desired segments into one or more of the VDMs, thereby  
 CC producing one or more desired product molecules (PMs). The methods can be  
 CC used for the efficient and specific recombination of NAM segments. They  
 CC can be used to generate chimeric DNA or RNA molecules that have the  
 CC desired characteristics and/or nucleic acid segments. The methods can  
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
 CC are used in the method of the invention

SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;  
 Best Local Similarity 56.0%; Pred. No. 12;  
 Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCGCTTYYKTRTACNAASTSG 25

Db 1 GTTCAGCTTCTTGTACAAAGTGT 25

RESULT 8

AAX78936

ID AAX78936 standard; DNA; 25 BP.

XX

AC AAX78936;

XX

DT 17-AUG-1999 (first entry)

XX

DE Oligonucleotide #2 for recombination and cloning method.

XX

KW Cloning; donor; recombination site; vector; chimeric; ss.

XX

OS Synthetic.

XX

PN WO9921977-A1.

XX

PD 06-MAY-1999.

XX

PF 26-OCT-1998; 98WO-US022589.

XX

PR 24-OCT-1997; 97US-0065930P.

XX

PR 23-OCT-1998; 98US-00177387.

XX

PA (LIFE-) LIFE TECHNOLOGIES INC.

XX

PI Hartley JL, Brasch MA, Temple GF, Fox DK;

XX

DR WPI; 1999-303011/25.

XX

PT New nucleic acid cloning methods.

XX

PS Disclosure; Page 159; 185pp; English.

XX

CC The invention relates to novel methods for cloning or subcloning one or  
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
 CC more desired nucleic acid segments flanked by at least 2 recombination  
 CC sites which do not recombine with each other; (2) one or more vector  
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
 CC not recombine with each other; and (3) one or more site-specific  
 CC recombination proteins; (b) incubating the combination to transfer one or  
 CC more of the desired segments into one or more of the VDMs, thereby  
 CC producing one or more desired product molecules (PMs). The methods can be  
 CC used for the efficient and specific recombination of NAM segments. They  
 CC can be used to generate chimeric DNA or RNA molecules that have the  
 CC desired characteristics and/or nucleic acid segments. The methods can  
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
 CC are used in the method of the invention

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;  
 Best Local Similarity 84.0%; Pred. No. 12;  
 Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCGCTTYYKTRTACNAASTSG 25

Db 1 AGCCWGCTTYYKTRTACNAAGTSG 25

RESULT 9

AAX78974

ID AAX78974 standard; DNA; 25 BP.

XX

AC AAX78974;

XX

DT 17-AUG-1999 (first entry)



```
XX Oligonucleotide #40 for recombination and cloning method.
DE Cloning; donor; recombination site; vector; chimeric; ss.
KW Synthetic.
OS WO9921977-A1.
XX WO9921977-A1.
XX 06-MAY-1999.
XX 26-OCT-1998; 98WO-US022589.
XX 24-OCT-1997; 97US-0065930P.
XX 23-OCT-1998; 98US-00177387.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA, Temple GP, Fox DK;
XX WPI; 1999-303011/25.
XX New nucleic acid cloning methods.
XX Disclosure; Page 170; 185pp; English.
XX The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NAME) comprising: (a) combining in vitro or
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
CC more desired nucleic acid segments flanked by at least 2 recombination
CC sites which do not recombine with each other; (2) one or more vector
CC donor molecules (VDMs) comprising at least 2 recombination sites which do
CC not recombine with each other; and (3) one or more site-specific
CC recombination proteins; (b) incubating the combination to transfer one or
CC more of the desired segments into one or more of the VDMs, thereby
CC producing one or more desired product molecules (PMs). The methods can be
CC used for the efficient and specific recombination of NAM segments. They
CC can be used to generate chimeric DNA or RNA molecules that have the
CC desired characteristics and/or nucleic acid segments. The methods can
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
CC are used in the method of the invention
XX SQ Sequence 25 BP; 4 A; 3 C; 3 G; 9 T; 0 U; 6 Other;
XX Query Match 78.4%; Score 19.6; DB 2; Length 25;
XX Best Local Similarity 72.0%; Pred. No. 12;
XX Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Oy 1 RKYCWGCTTTTKRTACNAASTSG 25
Db 1 ASCCWGCTTTTTRTACWAATSGW 25
RESULT 10
ID AAX78976 standard; DNA; 25 BP.
XX AAX78976;
XX 17-AUG-1999 (first entry)
XX Oligonucleotide #42 for recombination and cloning method.
DE Cloning; donor; recombination site; vector; chimeric; ss.
OS Synthetic.
XX WO9921977-A1.
XX 06-MAY-1999.
XX 26-OCT-1998; 98WO-US022589.
XX Query Match 78.4%; Score 19.6; DB 2; Length 25;
XX Best Local Similarity 72.0%; Pred. No. 12;
XX Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Oy 1 RKYCWGCTTTTKRTACNAASTSG 25
Db 1 ASCCWGCTTTTTRTACWAATSGW 25
RESULT 11
ID AAX78937 standard; DNA; 25 BP.
XX AAX78937;
XX 17-AUG-1999 (first entry)
XX Oligonucleotide #3 for recombination and cloning method.
DE Cloning; donor; recombination site; vector; chimeric; ss.
OS Synthetic.
XX WO9921977-A1.
XX 06-MAY-1999.
XX 26-OCT-1998; 98WO-US022589.
XX 24-OCT-1997; 97US-0065930P.
XX 23-OCT-1998; 98US-00177387.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA, Temple GP, Fox DK;
XX WPI; 1999-303011/25.
XX New nucleic acid cloning methods.
XX Disclosure; Page 159; 185pp; English.
XX
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CC The invention relates to novel methods for cloning or subcloning one or  
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
CC more desired nucleic acid segments flanked by at least 2 recombination  
CC sites which do not recombine with each other; (2) one or more vector  
CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
CC not recombine with each other; and (3) one or more site-specific  
CC recombination proteins; (b) incubating the combination to transfer one or  
CC more of the desired segments into one or more of the VDMs, thereby  
CC producing one or more desired product molecules (PMS). The methods can be  
CC used for the efficient and specific recombination of NAM segments. They  
CC can be used to generate chimeric DNA or RNA molecules that have the  
CC desired characteristics and/or nucleic acid segments. The methods can  
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
CC are used in the method of the invention

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;  
Best Local Similarity 76.0%; Pred. No. 12;  
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25  
Db 1 GTTCAGCTTTCRTACNAASTSG 25

## RESULT 12

AAX78935  
ID AAX78935 standard; DNA; 25 BP.

XX AC AAX78935;

XX DT 17-AUG-1999 (first entry)

XX DE Oligonucleotide #1 for recombination and cloning method.

XX KW Cloning; donor; recombination site; vector; chimeric; ss.

XX OS Synthetic.

XX PN WO9921977-A1.

XX PD 06-MAY-1999.

XX PF 26-OCT-1998; 98WO-US022589.

XX PR 24-OCT-1997; 97US-0065930P.

XX PR 23-OCT-1998; 98US-00177387.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;

XX DR WPI; 1999-303011/25.

XX PT New nucleic acid cloning methods.

XX PS Disclosure; Page 158; 185pp; English.

CC The invention relates to novel methods for cloning or subcloning one or  
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
CC more desired nucleic acid segments flanked by at least 2 recombination  
CC sites which do not recombine with each other; (2) one or more vector  
CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
CC not recombine with each other; and (3) one or more site-specific  
CC recombination proteins; (b) incubating the combination to transfer one or  
CC more of the desired segments into one or more of the VDMs, thereby  
CC producing one or more desired product molecules (PMS). The methods can be  
CC used for the efficient and specific recombination of NAM segments. They  
CC can be used to generate chimeric DNA or RNA molecules that have the  
CC desired characteristics and/or nucleic acid segments. The methods can

CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
CC are used in the method of the invention

XX SQ Sequence 25 BP; 3 A; 3 C; 2 G; 6 T; 0 U; 11 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25  
Db 1 RKYCWGCTTYYKTRTACNAASTSG 25

## RESULT 13

AAX78939  
ID AAX78939 standard; DNA; 25 BP.

XX AC AAX78939;

XX DT 17-AUG-1999 (first entry)

XX DE Oligonucleotide #5 for recombination and cloning method.

XX KW Cloning; donor; recombination site; vector; chimeric; ss.

XX OS Synthetic.

XX PN WO9921977-A1.

XX PD 06-MAY-1999.

XX PF 26-OCT-1998; 98WO-US022589.

XX PR 24-OCT-1997; 97US-0065930P.

XX PR 23-OCT-1998; 98US-00177387.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;

XX DR WPI; 1999-303011/25.

XX PT New nucleic acid cloning methods.

XX PS Disclosure; Page 159; 185pp; English.

CC The invention relates to novel methods for cloning or subcloning one or  
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
CC more desired nucleic acid segments flanked by at least 2 recombination  
CC sites which do not recombine with each other; (2) one or more vector  
CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
CC not recombine with each other; and (3) one or more site-specific  
CC recombination proteins; (b) incubating the combination to transfer one or  
CC more of the desired segments into one or more of the VDMs, thereby  
CC producing one or more desired product molecules (PMS). The methods can be  
CC used for the efficient and specific recombination of NAM segments. They  
CC can be used to generate chimeric DNA or RNA molecules that have the  
CC desired characteristics and/or nucleic acid segments. The methods can  
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
CC are used in the method of the invention

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;  
Best Local Similarity 80.0%; Pred. No. 12;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25  
Db 1 GTTCAGCTTYYKTRTACNAAGTSG 25

```
RESULT 14
AAS06185
ID AAS06185 standard; DNA; 25 BP.
XX
XX
AC AAS06185;
XX
DT 12-SEP-2001 (first entry)
XX
DE Phage-lambda recombination site attR2.
XX
XX Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
KW lambda integrase; therapeutic; ss.
XX
OS Bacteriophage lambda.
XX
XX WO200142509-A1.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US033546.
XX
XX 10-DEC-1999; 99US-0169983P.
XX
XX 09-MAR-2000; 2000US-0188020P.
XX
XX (CHEO/) CHEO D.
XX
XX (BRAS/) BRASCH M A.
XX
XX (TEMP/) TEMPLE G F.
XX
XX (HART/) HARTLEY J L.
XX
XX (BYRD/) BYRD D R N.
XX
XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
PI WPI; 2001-356174/37.
XX
DR Producing hybrid nucleic acids, useful for expressing novel therapeutic
XX polypeptides, by mixing the same or different nucleic acids having one or
PT more recombination sites in the presence of recombination proteins, e.g.
PT Cre.
XX
XX Disclosure; Fig 24A; 357pp; English.
XX
XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
CC nucleic acid sequences, and PCR primers of the invention. The att
CC sequences are recognised by the recombination protein lambda integrase
CC (Int). The invention is a new method of producing a population of hybrid
CC nucleic acids comprising mixing at least a first population of nucleic
CC acids comprising one or more recombination sites with at least one target
CC nucleic acid comprising one or more recombination sites and causing some
CC or all of the nucleic acids to recombine with all or some of the target
CC nucleic acids. The method is useful for producing a population of hybrid
CC nucleic acids which may be the same or different. The nucleic acids may
CC be used to express therapeutic proteins or peptides and they may also be
CC used to create novel fusion proteins by expressing different sequences
CC linked to each other. The method allows simultaneous cloning of two or
CC more different nucleic acids
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;
Query Match 78.4%; Score 19.6; DB 4; Length 25;
Best Local Similarity 56.0%; Pred. No. 12;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
QY 1 RKYCWGCTTYYKTRTACNAASTSG 25
DB 1 GTTCAGCTTCTTGTAACAAAGTGGT 25
Search completed: November 16, 2004, 04:02:44
Job time : 168.8 secs

RESULT 15
AAS06185
ID AAS06185 standard; DNA; 25 BP.
XX
XX
AC AAS06185;
XX
DT 12-SEP-2001 (first entry)
XX
DE Phage-lambda recombination site attR2.
XX
XX Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
KW lambda integrase; therapeutic; ss.
XX
OS Bacteriophage lambda.
XX
XX WO200142509-A1.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US033546.
XX
XX 10-DEC-1999; 99US-0169983P.
XX
XX 09-MAR-2000; 2000US-0188020P.
XX
XX (CHEO/) CHEO D.
XX
XX (BRAS/) BRASCH M A.
XX
XX (TEMP/) TEMPLE G F.
XX
XX (HART/) HARTLEY J L.
XX
XX (BYRD/) BYRD D R N.
XX
XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
PI WPI; 2001-356174/37.
XX
DR Producing hybrid nucleic acids, useful for expressing novel therapeutic
XX polypeptides, by mixing the same or different nucleic acids having one or
PT more recombination sites in the presence of recombination proteins, e.g.
PT Cre.
XX
XX Disclosure; Fig 24A; 357pp; English.
XX
XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
CC nucleic acid sequences, and PCR primers of the invention. The att
CC sequences are recognised by the recombination protein lambda integrase
CC (Int). The invention is a new method of producing a population of hybrid
CC nucleic acids comprising mixing at least a first population of nucleic
CC acids comprising one or more recombination sites with at least one target
CC nucleic acid comprising one or more recombination sites and causing some
CC or all of the nucleic acids to recombine with all or some of the target
CC nucleic acids. The method is useful for producing a population of hybrid
CC nucleic acids which may be the same or different. The nucleic acids may
CC be used to express therapeutic proteins or peptides and they may also be
CC used to create novel fusion proteins by expressing different sequences
CC linked to each other. The method allows simultaneous cloning of two or
CC more different nucleic acids
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;
Query Match 78.4%; Score 19.6; DB 4; Length 25;
Best Local Similarity 56.0%; Pred. No. 12;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
QY 1 RKYCWGCTTYYKTRTACNAASTSG 25
DB 1 GTTCAGCTTCTTGTAACAAAGTGGT 25
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Job time : 168.8 secs
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds  
(without alignments)  
494.978 Million cell updates/sec

Title: US-10-820-133-1

Perfect score: 25

Sequence: 1 rkycggttcttactnaastsgb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.6	78.4	25	3	US-09-233-493-1
2	19.6	78.4	25	3	US-09-233-493-2
3	19.6	78.4	25	3	US-09-233-493-3
4	19.6	78.4	25	3	US-09-233-493-4
5	19.6	78.4	25	3	US-09-233-493-5
6	19.6	78.4	25	3	US-09-005-476-1
7	19.6	78.4	25	3	US-09-005-476-2
8	19.6	78.4	25	3	US-09-005-476-3
9	19.6	78.4	25	3	US-09-005-476-4
10	19.6	78.4	25	3	US-09-005-476-5
11	19.6	78.4	25	3	US-09-233-492-1
12	19.6	78.4	25	3	US-09-233-492-2
13	19.6	78.4	25	3	US-09-233-492-3
14	19.6	78.4	25	3	US-09-233-492-4
15	19.6	78.4	25	3	US-09-233-492-5
16	19.6	78.4	25	3	US-09-296-280-1
17	19.6	78.4	25	3	US-09-296-280-2
18	19.6	78.4	25	3	US-09-296-280-3
19	19.6	78.4	25	3	US-09-296-280-4
20	19.6	78.4	25	3	US-09-296-280-5
21	19.6	78.4	25	3	US-09-296-280-11
22	19.6	78.4	25	3	US-09-296-280-40
23	19.6	78.4	25	3	US-09-296-280-42
24	19.6	78.4	25	4	US-09-498-074-1
25	19.6	78.4	25	4	US-09-498-074-2
26	19.6	78.4	25	4	US-09-498-074-3
27	19.6	78.4	25	4	US-09-498-074-4

28	19.6	78.4	25	4	US-09-498-074-5
29	19.6	78.4	25	4	US-09-498-074-1
30	19.6	78.4	25	4	US-09-498-074-2
31	19.6	78.4	25	4	US-09-498-074-3
32	19.6	78.4	25	4	US-09-498-074-4
33	19.6	78.4	25	4	US-09-498-074-5
34	19.6	78.4	25	5	PCT-US96-10082A-1
35	19.6	78.4	25	5	PCT-US96-10082A-2
36	19.6	78.4	25	5	PCT-US96-10082A-3
37	19.6	78.4	25	5	PCT-US96-10082A-4
38	19.6	78.4	25	5	PCT-US96-10082A-5
39	19.2	76.8	25	3	US-09-296-380-39
40	18.4	73.6	25	3	US-09-233-493-6
41	18.4	73.6	25	3	US-09-233-493-7
42	18.4	73.6	25	3	US-09-233-493-9
43	18.4	73.6	25	3	US-09-233-493-10
44	18.4	73.6	25	3	US-09-233-493-11
45	18.4	73.6	25	3	US-09-233-493-12

## ALIGNMENTS

### RESULT 1

US-09-233-493-1  
; Sequence 1, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; RECOMBINATION SITES  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
US-09-233-493-1

Sequence 5, Appli  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 39, Appli  
Sequence 6, Appli  
Sequence 7, Appli  
Sequence 9, Appli  
Sequence 10, Appli  
Sequence 11, Appli  
Sequence 12, Appli

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Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKYCWGCTTYYKTRTACNAASTSG 25
Db      1 RKYCWGCTTYYKTRTACNAASTSG 25

RESULT 2
US-09-233-493-2
; Sequence 2, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-233-493-2

Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.2;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKYCWGCTTYYKTRTACNAASTSG 25
Db      1 AGCCWGCTTYYKTRTACNAACTSG 25

RESULT 3
US-09-233-493-3
; Sequence 3, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/233,493  
FILING DATE: 20-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,476  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
US-09-233-493-4

Query Match 78.4%; Score 19.6; DB 3; Length 25;  
Best Local Similarity 80.0%; Pred. No. 1.2;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCGCTTYYKTRTACNAASTSG 25  
Db 1 AGCCGCTTCTCKTRTACNAAGTSG 25

RESULT 5  
US-09-233-493-5  
Sequence 5, Application US/09233493  
Patent No. 6143557  
GENERAL INFORMATION:  
APPLICANT: Hartley, James L.  
APPLICANT: Brasch, Michael A.  
TITLE OF INVENTION: Recombinational Cloning Using Engineered  
TITLE OF INVENTION: Recombination Sites  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
STREET: 1100 New York Ave., N. W. Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/233,493  
FILING DATE: 20-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,476  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
US-09-233-493-5  
Query Match 78.4%; Score 19.6; DB 3; Length 25;  
Best Local Similarity 80.0%; Pred. No. 1.2;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RKYCGCTTYYKTRTACNAASTSG 25  
Db 1 GTTCAGCTTYYKTRTACNAAGTSG 25

RESULT 6  
US-09-005-476-1  
Sequence 1, Application US/09005476  
Patent No. 6171861  
GENERAL INFORMATION:  
APPLICANT: Hartley, James L.  
APPLICANT: Brasch, Michael A.  
TITLE OF INVENTION: Recombinational Cloning Using Engineered  
TITLE OF INVENTION: Recombination Sites  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N. W. Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,476  
FILING DATE: herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
US-09-005-476-1

Query Match 78.4%; Score 19.6; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCGCTTYYKTRTACNAASTSG 25  
Db 1 RKYCGCTTYYKTRTACNAASTSG 25

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Db      1 RKYCWGCTTYYKTRTACNAASTSGB 25

RESULT 7
; Sequence 2, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; US-09-005-476-2

Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.2;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKYCWGCTTYYKTRTACNAASTSGB 25
      : : : : : : : : : : : : : : : : : :
Db      1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 8
; Sequence 3, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; US-09-005-476-3

Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.2;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKYCWGCTTYYKTRTACNAASTSGB 25
      : : : : : : : : : : : : : : : : : :
Db      1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 9
; Sequence 4, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; US-09-005-476-4

Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2;
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-3

Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.2;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKYCWGCTTYYKTRTACNAASTSGB 25
      : : : : : : : : : : : : : : : : : :
Db      1 GTTCAGCTTTCCTRTACNAACTSGB 25

RESULT 9
US-09-005-476-4
; Sequence 4, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-4

Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2;
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Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCGCTTYYKTRTACNAASTSGB 25  
:::|||||:|||||:|||||  
Db 1 AGCCWGCTTCKTRTACNAAGTSGB 25

RESULT 10  
US-09-005-476-5  
; Sequence 5, Application US/09005476  
; Patent No. 6171861  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/005,476  
; FILING DATE: herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
US-09-005-476-5

Query Match 78.4%; Score 19.6; DB 3; Length 25;  
Best Local Similarity 80.0%; Pred. No. 1.2;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCGCTTYYKTRTACNAASTSGB 25  
:::|||||:|||||:|||||  
Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

RESULT 11  
US-09-233-492-1  
; Sequence 1, Application US/09233492  
; Patent No. 6270969  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA

; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,492  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
US-09-233-492-1

Query Match 78.4%; Score 19.6; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCGCTTYYKTRTACNAASTSGB 25  
|||||:|||||:|||||  
Db 1 RKYCGCTTYYKTRTACNAASTSGB 25

RESULT 12  
US-09-233-492-2  
; Sequence 2, Application US/09233492  
; Patent No. 6270969  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,492  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-2
Query Match 78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.2;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTKTRTACNAAGTSG 25
Db 1 AGCCWGCCTTTTKTRTACNAAGTSG 25

RESULT 13
US-09-233-492-3
; Sequence 3, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-4
Query Match 78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTKTRTACNAAGTSG 25
Db 1 AGCCWGCCTTTTKTRTACNAAGTSG 25

RESULT 14
US-09-233-492-4
; Sequence 4, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-5
Query Match 78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTKTRTACNAAGTSG 25
Db 1 AGCCWGCCTTTTKTRTACNAAGTSG 25

RESULT 15
US-09-233-492-5
; Sequence 5, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
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; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-492-5

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Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. NO. 1.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RKYCWGCTTYYKTRTACNAAGTSG 25
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Db 1 GTTAGCTTYYKTRTACNAAGTSG 25

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Search completed: November 16, 2004, 10:22:29  
Job time : 35.9 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 : Search time 314 Seconds  
(without alignments)  
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Title: US-10-820-133-1

Perfect score: 25

Sequence: 1 rkycwgttttyktrtacnaastsgb 25

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Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	19.6	78.4	25	9	US-09-855-797A-1
3	19.6	78.4	25	9	US-09-855-797A-2
4	19.6	78.4	25	9	US-09-855-797A-3
5	19.6	78.4	25	9	US-09-855-797A-4
6	19.6	78.4	25	9	US-09-855-797A-5
7	19.6	78.4	25	9	US-09-855-797A-11
8	19.6	78.4	25	9	US-09-855-797A-40
9	19.6	78.4	25	9	US-09-855-797A-42
10	19.6	78.4	25	9	US-09-822-634-4
11	19.6	78.4	25	9	US-09-822-634-5
12	19.6	78.4	25	9	US-09-907-900-1

13	19.6	78.4	25	9	US-09-907-900-2	Sequence 2, Appli
14	19.6	78.4	25	9	US-09-907-900-3	Sequence 3, Appli
15	19.6	78.4	25	9	US-09-907-900-4	Sequence 4, Appli
16	19.6	78.4	25	9	US-09-907-900-5	Sequence 5, Appli
17	19.6	78.4	25	9	US-09-907-900-11	Sequence 11, Appli
18	19.6	78.4	25	9	US-09-907-900-40	Sequence 40, Appli
19	19.6	78.4	25	9	US-09-907-900-42	Sequence 42, Appli
20	19.6	78.4	25	9	US-09-907-719-1	Sequence 1, Appli
21	19.6	78.4	25	9	US-09-907-719-2	Sequence 2, Appli
22	19.6	78.4	25	9	US-09-907-719-3	Sequence 3, Appli
23	19.6	78.4	25	9	US-09-907-719-4	Sequence 4, Appli
24	19.6	78.4	25	9	US-09-907-719-5	Sequence 5, Appli
25	19.6	78.4	25	9	US-09-907-719-11	Sequence 11, Appli
26	19.6	78.4	25	9	US-09-907-719-40	Sequence 40, Appli
27	19.6	78.4	25	9	US-09-907-719-42	Sequence 42, Appli
28	19.6	78.4	25	10	US-09-432-085-1	Sequence 1, Appli
29	19.6	78.4	25	10	US-09-432-085-2	Sequence 2, Appli
30	19.6	78.4	25	10	US-09-432-085-3	Sequence 3, Appli
31	19.6	78.4	25	10	US-09-432-085-4	Sequence 4, Appli
32	19.6	78.4	25	10	US-09-432-085-5	Sequence 5, Appli
33	19.6	78.4	25	10	US-09-985-448-1	Sequence 1, Appli
34	19.6	78.4	25	10	US-09-985-448-2	Sequence 2, Appli
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36	19.6	78.4	25	10	US-09-985-448-4	Sequence 4, Appli
37	19.6	78.4	25	10	US-09-985-448-5	Sequence 5, Appli
38	19.6	78.4	25	10	US-09-985-448-11	Sequence 11, Appli
39	19.6	78.4	25	10	US-09-985-448-40	Sequence 40, Appli
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41	19.6	78.4	25	14	US-10-058-292-1	Sequence 1, Appli
42	19.6	78.4	25	14	US-10-058-292-2	Sequence 2, Appli
43	19.6	78.4	25	14	US-10-058-292-3	Sequence 3, Appli
44	19.6	78.4	25	14	US-10-058-292-4	Sequence 4, Appli
45	19.6	78.4	25	14	US-10-058-292-5	Sequence 5, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-732-914-12  
; Sequence 12, Application US/09732914  
; Patent No. US20020007051A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheo, David  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Hartley, James L.  
; APPLICANT: Byrd, Devon R.N.  
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in  
; TITLE OF INVENTION: Recombinational Cloning  
; FILE REFERENCE: 0942.5010002  
; CURRENT APPLICATION NUMBER: US/09/732.914  
; CURRENT FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 60/169,983  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: US 60/188,020  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: attr2  
US-09-732-914-12

Query Match 78.4%; Score 19.6; DB 9; Length 25;  
Best Local Similarity 56.0%; Pred. No. 9.2;  
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTYKTRTACNAASTSGB 25

Db 1 GTTCAGCTTCTTGTACAAAGTGT 25

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RESULT 2
US-09-855-797A-1
; Sequence 1, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-1

Query Match      78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKYCWGCTTTTKTRTACNAASTSG 25
Db      1 RKYCWGCTTTTKTRTACNAASTSG 25

RESULT 3
US-09-855-797A-2
; Sequence 2, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-2

Query Match      78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKYCWGCTTTTKTRTACNAASTSG 25
Db      1 RKYCWGCTTTTKTRTACNAASTSG 25
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Query Match      78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 84.0%; Pred. No. 9.2;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKYCWGCTTTTKTRTACNAASTSG 25
Db      1 AGCCWGCTTTTKTRTACNAACTSG 25

RESULT 4
US-09-855-797A-3
; Sequence 3, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-3

Query Match      78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 9.2;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKYCWGCTTTTKTRTACNAASTSG 25
Db      1 GTTCAGCTTTCKTRTACNAACTSG 25

RESULT 5
US-09-855-797A-4
; Sequence 4, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-4

Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25
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Db 1 AGCCWGCCTTCKTRTACNAAGTSGB 25

RESULT 6
US-09-855-797A-5
; Sequence 5, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-5

Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25
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Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

RESULT 7
US-09-855-797A-11
; Sequence 11, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
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; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-11

Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 56.0%; Pred. No. 9.2;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25
   ::::|||||:|||||:|||||:|||||:
Db 1 GTTCAGCTTCTTGTACAAAGTGCT 25

RESULT 8
US-09-855-797A-40
; Sequence 40, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-40

Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 72.0%; Pred. No. 9.2;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25
   ::::|||||:|||||:|||||:|||||:
Db 1 ASCCWGCTTYYKTRTACWAASTRGW 25

RESULT 9
US-09-855-797A-42
; Sequence 42, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
```

```

; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-42

```

```

Query Match      78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 68.0%; Pred. No. 9.2;
Matches 17; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 RKYCWGCTTTTKTRTACNAASTSG 25
   ::::|||||:|||||:|||||:
Db 1 GTTCAGCTTTTKTRTACWAATSGW 25

```

```

RESULT 10
US-09-822-634-4
; Sequence 4, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-09-822-634-4

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```

Query Match      78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 9.2;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 RKYCWGCTTTTKTRTACNAASTSG 25
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Db 1 GTTCAGCTTTTKTRTACNAACTSG 25

```

```

RESULT 11
US-09-822-634-5
; Sequence 5, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin

```

```

; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-09-822-634-5

```

```

Query Match      78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RKYCWGCTTTTKTRTACNAASTSG 25
   ::::|||||:|||||:|||||:
Db 1 AGCCWGGCTTTCKTRTACNAAGTSG 25

```

```

RESULT 12
US-09-907-900-1
; Sequence 1, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-1

```

```

Query Match      78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RKYCWGCTTTTKTRTACNAASTSG 25
   |||||:|||||:|||||:|||||:
Db 1 RKYCWGCTTTTKTRTACNAASTSG 25

```

```

RESULT 13
US-09-907-900-2
; Sequence 2, Application US/09907900

```



```
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-2
```

```
Query Match      78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 84.0%; Pred. No. 9.2;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25
   ::::::::::::::::::::::::::::
Db 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
```

```
RESULT 14
US-09-907-900-3
; Sequence 3, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-3
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```
Query Match      78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 9.2;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25
   ::::::::::::::::::::::::::::::
Db 1 GTTCAGCTTTCCKTRTACNAACTSGB 25
```

```
RESULT 15
US-09-907-900-4
; Sequence 4, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-4
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```
Query Match      78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25
   ::::::::::::::::::::::::::::::
Db 1 AGCCWGCCTTTCCKTRTACNAAGTSGB 25
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Search completed: November 16, 2004, 11:14:57
Job time : 314.1 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds  
(without alignments)  
594.643 Million cell updates/sec

Title: US-10-820-133-1

Perfect score: 25

Sequence: 1 rkywgttttyktrtaacnaatsgb 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821986598 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gse1: \*  
9: gb\_gse2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.6	78.4	321	2	BF086649 CM0-GN007
2	19.6	78.4	595	2	AW993039 RC2-BN003
3	19.6	78.4	635	7	CN484020 hw41b03.Y
C 4	19.6	78.4	672	8	AQ990864 Rfc01701
5	19.6	78.4	706	4	B1836912 603084230
6	19.6	78.4	714	5	BX359053 BX359053
7	19.6	78.4	752	4	BG620766 602617479
C 8	19.6	78.4	753	8	AQ990861 Rfc01698
9	19.6	78.4	797	4	BG427603 602497040
10	19.6	78.4	805	7	CF629462 DKFZp469K
C 11	19.6	78.4	808	8	AQ990388 Rfc01153
12	19.6	78.4	810	5	BQ216337 AGENCOURT
13	19.6	78.4	824	4	BG620383 602617507
14	19.6	78.4	831	5	BQ230007 AGENCOURT
15	19.6	78.4	852	4	BG401996 602466712
16	19.6	78.4	855	2	BE785867 601478671
17	19.6	78.4	856	2	BE893159 604337059
18	19.6	78.4	859	5	BX398237 BX398237
19	19.6	78.4	862	2	BE895530 601438319
20	19.6	78.4	888	7	CK209237 FGAS02099
21	19.6	78.4	908	4	BT546971 603190186
22	19.6	78.4	954	5	BQ893686 AGENCOURT
23	19.6	78.4	986	5	BX398580 BX398580
24	19.6	78.4	994	4	BM804936 AGENCOURT

25	19.6	78.4	994	7	CK162659 FGAS01525
26	19.6	78.4	1012	7	CK211630 FGAS02348
27	19.6	78.4	1019	2	BE300319 600944384
28	19.6	78.4	1031	7	CK163965 FGAS01660
29	19.6	78.4	1031	7	CK212789 FGAS02467
30	19.6	78.4	1043	7	CK212830 FGAS02472
31	19.6	78.4	1051	7	CK212815 FGAS02470
32	19.6	78.4	1053	7	CK212320 FGAS02419
33	19.6	78.4	1059	7	CK163940 FGAS01658
34	19.6	78.4	1062	7	CK212429 FGAS02430
35	19.6	78.4	1067	7	CK212431 FGAS02430
36	19.6	78.4	1070	7	CK213073 FGAS02497
37	19.6	78.4	1071	7	CK211886 FGAS02374
38	19.6	78.4	1071	7	CK212465 FGAS02433
39	19.6	78.4	1076	7	CK216054 FGAS02803
40	19.6	78.4	1076	7	CK217224 FGAS02922
41	19.6	78.4	1082	7	CK212170 FGAS02403
42	19.6	78.4	1088	7	CK205724 FGAS01725
43	19.6	78.4	1093	7	CK211774 FGAS02362
44	19.6	78.4	1095	7	CK212335 FGAS02420
45	19.6	78.4	1098	7	CK213245 FGAS02515

#### ALIGNMENTS

RESULT 1  
BF086649/c  
LOCUS BF086649 321 bp mRNA linear EST 19-OCT-2000  
DEFINITION CM0-GN0077-160900-559-g06 GN0077 Homo sapiens CDNA, mRNA sequence.  
ACCESSION BF086649  
VERSION BF086649.1 GI:108922268  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,  
Goldman, G.H., Carvalho, A.P., Mateukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=CM0-GN0077-160  
900-559-g06&tl=2000-09-16&tl=1)  
Seq primer: puc 18 forward  
High quality sequence start: 12  
High quality sequence stop: 321.

#### FEATURES

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1..321  
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/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="GN0077"

/notes="Organ: placenta\_normal; Vector: puc18; Site: 1;  
SmaI; Site 2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

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Query Match      78.48; Score 19.6; DB 2; Length 321;
Best Local Similarity 56.08; Pred.No. 1.3e+02;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY      1 RKYCWGCTTTTXYRTACNAASTGB 25
Db      186 GTTCTGTTTCTTATACCAAGTGC 162

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RESULT 2	AM993039	595 bp	mRNA	linear	EST 05-JUN-2000
LOCUS	RC2-BN0033-060200-012-c06 BN0033		Homo sapiens	cdNA,	mRNA sequence.
DEFINITION	AM993039				
ACCESSION	AM993039.1	GI:8253175			
VERSION	EST.				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1. (bases 1 to 595)				
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Brines,M.R., Naga,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.				

## ORIGIN

Query Match	78.4%	Score 19.6;	DB 2;	Length 595;
Best Local Similarity	56.0%;	Pred. No. 1.4e+02;		
Matches 14:	Conservative	10: Mismatches	1: Indels	0: Gaps

**Oy**      1 PKYCWGCTTYYKTRTACNAASTSGB 25  
          :::|::|::|::|::|::|::|::|::|::|:  
**Dβ**      88 GTTCTGTCTTTCTTATACCAGTGTC 112

RESULT 3	ACCESSION
CN484020	VERSION
LOCUS	KEYWORDS
DEFINITION	SOURCE
	ORGANISM

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 635)  
REFERENCE Tsai, J.Y. and Wistow, G.  
AUTHORS

**JOURNAL  
COMMENT**

CONTACT: WISLOW G  
Section on Molecular Structure and Funct  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: [graeme@helix.nih.gov](mailto:graeme@helix.nih.gov)  
 Plate: 41 row: b column: c  
 Seg primer: M13p1 reverse

FEATURES	SOURCE
1. The first 100 words of the text are the most important.	1. The first 100 words of the text are the most important.
2. The first 100 words of the text are the most important.	2. The first 100 words of the text are the most important.
3. The first 100 words of the text are the most important.	3. The first 100 words of the text are the most important.
4. The first 100 words of the text are the most important.	4. The first 100 words of the text are the most important.
5. The first 100 words of the text are the most important.	5. The first 100 words of the text are the most important.
6. The first 100 words of the text are the most important.	6. The first 100 words of the text are the most important.
7. The first 100 words of the text are the most important.	7. The first 100 words of the text are the most important.
8. The first 100 words of the text are the most important.	8. The first 100 words of the text are the most important.
9. The first 100 words of the text are the most important.	9. The first 100 words of the text are the most important.
10. The first 100 words of the text are the most important.	10. The first 100 words of the text are the most important.

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hw41b03"
/cell_type="pericytes"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human primary human ocular pericytes.
Unamplified (hw)"
/note="Organ: Eye; Vector: pSPORT1; RNA was extracted from
primary human pericytes in culture. A directionally cloned
cDNA library in the pSPORT1 vector (Invitrogen) was
constructed at Bioserve Biotechnology (Laurel MD)
essentially following the protocols of the SuperScript
Plasmid System full details of which are contained in the
manufacturer's instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adaptor
[5'-pGACTAGTTCCTAGATCGCGGCGGCC(T)15-3']. cDNA was
cloned in Not I/Sal I sites. EST analysis was performed at
the NTH Intramural Sequencing Center (NISC)"

```

## ORIGIN

Query Match	78.4%	Score 19.6;	DB 7;	Length 635;
Best Local Similarity	56.0%;	Pred. No. 1.5e+02;		
Matches 14;	Conservative 10;	Mismatches 1;	Indels 0;	Gaps 0;

RESULT 4  
AO990864/

LOCUS	AQ990864	672 bp	DNA	linear	GSS 14-AUG-2000
DEFINITION	RC01701 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01701, genomic survey sequence.				
ACCESSION	AQ990864				

LOCUS	AQ990864	672 bp	DNA	linear	GSS 14-AUG-2000
DEFINITION	RC01701 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01701, genomic survey sequence.				
ACCESSION	AQ990864				

LOCUS	AQ990864	672 bp	DNA	linear	GSS 14-AUG-2000
DEFINITION	RC01701 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01701, genomic survey sequence.				
ACCESSION	AQ990864				

```

VERSION      AQ990864.1  GI:9649458
KEYWORDS     GSS.
SOURCE       Photorhabdus luminescens
ORGANISM     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
              Enterobacteriaceae; Photorhabdus.
REFERENCE    1 (bases 1 to 672)
AUTHORS      ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
              Daborn,P.O., Bowen,D. and Biattnier,F.R.
TITLE        A genomic sample sequence of the entomopathogenic bacterium
              Photorhabdus luminescens W14: potential implications for virulence
JOURNAL      Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE      20378633
PUBMED       10319786
COMMENT      Contact: ffrench-Constant RH
              Department of Biology and Biochemistry
              University of Bath
              South Building, Bath BA2 7AY, UK
              Tel: (44) 1225 826621
              Fax: (44) 1225 826779
              Email: bsrf@bath.ac.uk
              This is one of 2,122 random reads from the M13 library. For
              annotation of identified clones (BLASTX, BLASTN and mapping to E.
              coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
              Acids Res.
Seq primer:  M13 Forward
Class:       shotgun.
FEATURES     source
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                /organism="Photorhabdus luminescens"
                /mol_type="genomic DNA"
                /strain="W14"
                /db_xref="taxon:29488"
                /clone="P1G01701"
                /dev_stages="Primary phase variant"
                /clone_lib="Photorhabdus luminescens strain W14 M13
                library"
                /note="Genomic DNA from strain W14 was size selected (1-2
                kb) and then cloned into M13 Janus."
ORIGIN
Query Match      78.4%; Score 19.6; DB 8; Length 672;
Best Local Similarity 56.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCGCTTTTKRTACNAASTSGB 25
    ::::::::::::::::::::
Db 637 GTTCAGCTTTTATCTACTAGTGC 613

RESULT 5
BI836912      706 bp mRNA linear EST 04-OCT-2001
LOCUS         603084230F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5223318 5',
DEFINITION    mRNA sequence.
ACCESSION     BI836912
VERSION       BI836912.1 GI:15948462
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 706)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgsaps-remail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be

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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1561 row: 1 column: 07
High quality sequence stop: 646.
Location/Qualifiers
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  /organism="Homo sapiens"
  /mol_type="mRNA"
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  /clone="IMAGE:5223318"
  /lab_host="DH10B"
  /clone_lib="NIH_MGC_120"
  /note="Organ: pooled pancreas and spleen; Vector:
  pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
  source anonymous pool of spleen and pancreas from 28 yo
  male. Library is oligo-dT primed and directionally cloned
  (EcoRV site is destroyed upon cloning). Average insert
  size 1.5 kb, insert size range 1-2.5 kb. Library is
  normalized and enriched for full-length clones and was
  constructed by C. Gruber (Invitrogen). Research Genetics
  tracking code 025. Note: this is a NIH_MGC Library."
ORIGIN
Query Match      78.4%; Score 19.6; DB 4; Length 706;
Best Local Similarity 56.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCGCTTTTKRTACNAASTSGB 25
    ::::::::::::::::::::
Db 269 GTTCGTCTTCTTATACCAAGTGC 293

RESULT 6
BX359053      714 bp mRNA linear EST 08-APR-2004
LOCUS         BX359053 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
DEFINITION    Clone CSODI052YG13 5-PRIME, mRNA sequence.
ACCESSION     BX359053
VERSION       BX359053.2 GI:46291338
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 714)
AUTHORS      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL       Unpublished (2001)
COMMENT      On May 5, 2003 this sequence version replaced gi:30372318.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life technologies, a
              division of Invitrogen. This sequence belongs to sequence cluster
              470.r
              For more information about this cluster, see
              http://www.genoscope.cns.fr/cdna/s=CSODI052AD07QPI&c=470.r.
              Location/Qualifiers
                1..714
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CSODI052YG13"
                /tissue_type="PLACENTA COT 25-NORMALIZED"
                /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
FEATURES     source
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              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
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              /note="1st strand cDNA was primed with a NotI-oligo(dT)
              primer. Five prime end enriched, double-strand cDNA was
              digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MCC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLC1356 row: p column: 10  
 High quality sequence stop: 703.

Location/Qualifiers  
 1. .797

## FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4610937"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MCC_75"
/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggccattatggcc); Site:2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCATATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGGCGCGAGCGCGGCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MCC Library."
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## ORIGIN

Query Match 78.4%; Score 19.6; DB 4; Length 797;  
 Best Local Similarity 56.0%; Pred. No. 1.5e+02;  
 Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25

Db 429 GTTCGTCTTCTTATACCAAGTGGC 453

## RESULT 10

CR629462 805 bp mRNA linear EST 11-AUG-2004  
 LOCUS  
 DEFINITION DKFPZ469K1521\_r1\_469 (synonym: pkidi) Pongo pygmaeus cDNA clone  
 DKFPZ469K1521\_5', mRNA sequence.

CR629462

CR629462.1 GI:51125542

EST.

Pongo pygmaeus (orangutan)

ORGANISM

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

1 (bases 1 to 805)

Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,

Fobo, G., Han, M. and Wiemann, S.

Pongo pygmaeus mRNA (Bahr, A., Lauber, J., Mewes, H.W., et al.)

Unpublished (2004)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert from S. Wiemann,  
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);  
 Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen  
 (Hilden/Germany) within the cDNA sequencing consortium of the  
 German Genome Project. This clone (DKFPZ469K1521) is available at  
 the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
 Berlin, Germany. Please contact RZPD for ordering:  
<http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFPZ469K1521>  
 Further information about the clone and the sequencing project is  
 available at <http://mips.gsf.de/projects/cdna/>.

## FEATURES

source

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Location/Qualifiers
1. .805
/organism="Pongo pygmaeus"
/mol_type="mRNA"
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/clone="DKFPZ469K1521"
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/dev_stage="adult"
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/lab_host="DH10B"
/clone_lib="469 (synonym: pkidi)"
/notes="vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"
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## ORIGIN

Query Match 78.4%; Score 19.6; DB 7; Length 805;  
 Best Local Similarity 56.0%; Pred. No. 1.5e+02;  
 Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25

Db 543 GTTCGTCTTCTTATACCAAGTGGC 567

## RESULT 11

AQ990388/c

LOCUS

DEFINITION Rf01153 Photorhabdus luminescens strain W14 M13 library  
 Photorhabdus luminescens genomic clone PLG01153, genomic survey  
 sequence.

ACCESSION AQ990388

VERSION AQ990388.1 GI:9648982

KEYWORDS GSS.

SOURCE

ORGANISM

Photorhabdus luminescens  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Photorhabdus.

1 (bases 1 to 808)

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

20378633

10919786

Contact: ffrench-Constant RH

Department of Biology and Biochemistry

University of Bath

South Building, Bath BA2 7AY, UK

Tel: (44) 1225 826621

Fax: (44) 1225 826779

Email: bsr@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For  
 annotation of identified clones (BLASTX, BLASTN and mapping to E.

coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic

Acids Res.

Seq primer: M13 Forward

Class: shotgun.

Location/Qualifiers

1. .808

/organism="Photorhabdus luminescens"

/mol\_type="genomic DNA"

/strain="W14"

/db\_xref="taxon:29488"

/clone="PLG01153"

/dev\_stage="primary phase variant"

/clone\_lib="Photorhabdus luminescens strain W14 M13

library"

/notes="Genomic DNA from strain W14 was size selected (1-2

kb) and then cloned into M13 Janus."

## ORIGIN

Query Match 78.4%; Score 19.6; DB 8; Length 808;  
 Best Local Similarity 56.0%; Pred. No. 1.5e+02;  
 Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25

Db 628 GTTCAGCTTTTATATACTAAGTGGC 604

## RESULT 12

BQ216337





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Query Match      78.4%; Score 19.6; DB 5; Length 831;
Best Local Similarity 56.0%; Pred. No. 1.5e+00;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY      1 RKYCWGCTTYYKTRTCNNAASTGB 25
Db      567 GTTCTGCTTCTTATACCAAGTGCC 591

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RESULT 15	852 bp	mRNA	linear	EST 12-MAR-2001		
BG401996	602466712F1	NIH_MGC_75	Homo sapiens	CDNA clone IWAG:4594610 5',		
LOCUS	mRNA sequence.					
DEFINITION	mRNA sequence.					
ACCESSION	BG401996					
VERSION	1	GI:13295444				
KEYWORDS	EST.					
SOURCE	BG401996.1					
ORGANISM	Homo sapiens (human)					
REFERENCE	Homo sapiens					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
JOURNAL	1 (bases 1 to 852)					
COMMENT	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .					
	National Institutes of Health, Mammalian Gene Collection (MGC)					
	Unpublished (1999)					
	Contact: Robert Strausberg, Ph.D.					
	Email: <a href="mailto:csapbs@email.nih.gov">csapbs@email.nih.gov</a>					
	Tissue Procurement: CLONTECH Laboratories, Inc.					
	CDNA Library Preparation: CLONTECH Laboratories, Inc.					
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
	DNA Sequencing by: Incyte Genomics, Inc.					
	Clone distribution: MGC clone distribution information can be					
	found through the I.M.A.G.E. Consortium/LLNL at:					
	<a href="http://image.llnl.gov">http://image.llnl.gov</a>					
	Plate: LLCW1336	row: h	column: 03			
	High quality sequence	stop: 591.				

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/clone_lib="NIH_MGC_75"
/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgccgtccgcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGGGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

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ORIGIN

Query Match 78.4%; Score 19.6; DB 4; Length 852;  
Best Local Similarity 56.0%; Pred. No. 1.5e+03;  
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKYCWGCTTYYKTRKTACNAASTGBB 25  
:::|||||:::|||||:::|:  
DB 409 GTTCTGCTTCTTATACCAAGTGC 433  
:::|||||:::|||||:::|:

CAI: NOTE: THIS IS A NARFLOC LIBRARY.

Search completed: November 16, 2004, 10:16:27  
Job time : 1536 secs

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Result No.	Score	Query		DB	ID	Description
		Match	%			
C	1	21.2	84.8	25	6	AR124522 Sequence
	2	21.2	84.8	25	6	AR163173 Sequence
	3	21.2	84.8	25	6	AR493774 Sequence
	4	21.2	84.8	25	6	AX491641 Sequence
	5	21.2	84.8	25	6	AX498612 Sequence
	6	21.2	84.8	25	6	BD131328 Recombinant
	7	21.2	84.8	237955	10	AC122669 Rattus norvegicus
	8	21.2	84.8	256498	2	AC118339 Rattus norvegicus
	9	21.2	84.8	383259	2	AC121737 Rattus norvegicus
C	10	21	84.0	137122	10	AC123037 Mus musculus
	11	21	84.0	198872	9	AC147382 Pan troglodytes
	12	21	84.0	20431	2	AC125159 Mus musculus
	13	20.4	81.6	25	6	BD131366 Recombinant
	14	20	80.0	25	6	AR124526 Sequence
	15	20	80.0	25	6	AR124527 Sequence
	16	20	80.0	25	6	AR124553 Sequence
	17	20	80.0	25	6	AR124554 Sequence
	18	20	80.0	25	6	AR163177 Sequence
19	20	80.0	25	6	AR163178 Sequence	

RESULT	2
AR163173	
LOCUS	25 bp DNA linear PAT 17-OCT-2001
DEFINITION	Sequence 2 from patent US 6270969.
ACCESSION	AR163173
VERSION	AR163173.1 GI:16233679
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 25)
TITLE	Hartley,J.L. and Brasch,M.A. Recombinational cloning using engineered recombination sites

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  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCCGCTTTTKTRTACNAACTSGB 25
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    |||
RESULT 3
AR493774 AR493774 25 bp mRNA linear PAT 15-MAY-2004
LOCUS Sequence 2 from patent US 6720140.
DEFINITION
ACCESSION AR493774
VERSION AR493774.1 GI:47266184
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 2 13-APR-2004;
FEATURES Location/Qualifiers
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  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCCGCTTTTKTRTACNAACTSGB 25
    |||
Db 1 AGCCGCTTTTKTRTACNAACTSGB 25
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RESULT 4
AX491641 AX491641 25 bp DNA linear PAT 16-AUG-2002
LOCUS Sequence 2 from Patent EP1227147.
DEFINITION
ACCESSION AX491641
VERSION AX491641.1 GI:22324149
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 2 31-JUL-2002;
FEATURES Location/Qualifiers
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Db 1 AGCCGCTTTTKTRTACNAACTSGB 25
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LOCUS Sequence 2 from Patent EP1229113.
DEFINITION
ACCESSION AX498612
VERSION AX498612.1 GI:23343409
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 2 07-AUG-2002;
FEATURES Location/Qualifiers
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  Best Local Similarity 100.0%; Pred. No. 11;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCCGCTTTTKTRTACNAACTSGB 25
    |||
Db 1 AGCCGCTTTTKTRTACNAACTSGB 25
    |||
RESULT 6
BD131328 BD131328 25 bp DNA linear PAT 18-SEP-2002
LOCUS Recombinational cloning using nucleic acids having recombination
DEFINITION sites.
ACCESSION BD131328
VERSION BD131328.1 GI:23226273
KEYWORDS JP 2002500861-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 2 15-JAN-2002;
COMMENT LIFE TECHNOLOGIES INC
OS Unknown
PN JP 2002500861-A/2
PD 15-JAN-2002
PR 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
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  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCCGCTTTTKTRTACNAACTSGB 25
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Db      1  ||||||| 1 ACCGCGCTTTKTRACNACTSGB 25

RESULT 7
AC122669/c
LOCUS   AC122669
DEFINITION Rattus norvegicus 4 BAC CH230-172C22 (Children's Hospital Oakland Research Institute) complete sequence.
ACCESSION AC122669
VERSION   AC122669.6 GI:49457875
KEYWORDS  HTG.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus

REFERENCE
AUTHORS   1 (bases 1 to 227955)
           Murzyn,D.Marie., Metzker,M.Lee., Abranzon,S., Adams,C., Alder,J.,
           Allen,C., Allen,H., Albrooks,S., Amin,A., Anguiano,D.,
           Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
           Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
           Biswalto,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
           Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,B.,
           Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
           Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
           Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
           Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
           Delgado,O., Denson,S., Detamo,C., Ding,Y., Dinh,H., Divya,K.,
           Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
           Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
           Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
           Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
           Gebrgeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
           Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
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           Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
           Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
           Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
           Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
           Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
           Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
           Lorensuhewa,L., Louisleged,H., Lozado,R.J., Lu,X., Ma,J.,
           Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
           Mangun,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
           Mawhinney,S., McLeod,M., McNeill,T., Meenen,E., Milosavljevic,A.,
           Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,
           Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D.,
           Newton,N., Nguyen,N., Norris,S., Nwaokemelehen,O., Okwuonu,G.,
           Olarunpungoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,
           Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A.,
           Popovic,D., Primus,E., Pu.L.-L., Puazo,M., Quiroz,J., Rachlin,E.,
           Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,
           Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A.,
           Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S.,
           Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,
           Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E.,
           Song,X.-Z., Sorelle,R., Soea,J., Steimle,M., Strong,R., Sutton,A.,
           Tatek,A., Tabar,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
           Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D.,
           Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J.,
           Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wlecszyk,R.,
           Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
           Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
           Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
           Holt,R.A., Smith,H.O., Weinstein,G. and Gibbs,R.A.
           Direct Submission
           Unpublished
           2 (bases 1 to 227955)
           Worley,K.C.
REFERENCE
AUTHORS   Direct Submission
TITLE     Submitted (25-MAY-2002) Human Genome Sequencing Center, Department
JOURNAL   of Molecular and Human Genetics, Baylor College of Medicine, One
          Bay Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS   Rat Genome Sequencing Consortium
TITLE     Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
JOURNAL   of Molecular and Human Genetics, Baylor College of Medicine, One
          Bay Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS   Direct Submission
TITLE     Submitted (24-JUN-2004) Human Genome Sequencing Center, Department
JOURNAL   of Molecular and Human Genetics, Baylor College of Medicine, One
          Bay Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS   Direct Submission
TITLE     Submitted (30-JUN-2004) Human Genome Sequencing Center, Department
JOURNAL   of Molecular and Human Genetics, Baylor College of Medicine, One
          Bay Plaza, Houston, TX 77030, USA

COMMENT   On Jun 30, 2004 this sequence version replaced gi:49170124.
          Sequencing is completed to a minimum standard of double strand
          coverage with a minimum of 2 clones and 2 reads with no ambiguities
          or 2 chemistries with a minimum of 2 clones and 3 reads with no
          ambiguities. If the sequence quality does not meet this standard,
          it will be indicated in the annotation.

FEATURES
          source
            1. 227955
               /organism="Rattus norvegicus"
               /mol_type="genomic DNA"
               /db_xref="taxon:10116"
               /chromosome="4"
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               183..359
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               360..404
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               409..548
               /rpt_family="B1_Mur1"
               832..1220
               /rpt_family="L1_Rat3"
               2104..2396
               /rpt_family="Tigger7"
               2410..2605
               /rpt_family="Tigger7"
               complement(2606..2686)
               /rpt_family="ID4_"
               2687..2802
               /rpt_family="Tigger7"
               2821..2930
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               3584..3691
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               3692..3785
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               3786..3939
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               3945..3989
               /rpt_family="B4"
               4075..4186
               /rpt_family="PB1D10"
               4269..4290
               /rpt_family="AT_rich"
               4362..4409
               /rpt_family="(TC)n"
               4409..4600
               /rpt_family="(TG)n"
               complement(4702..4845)
               /rpt_family="ID_B1"
               4917..4942
               /rpt_family="(TTTTG)n"

```



Baylor Plaza, Houston, TX 77030, USA  
 On Oct 9, 2002 this sequence version replaced gi:21746207.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GRVC  
 Center clone name: CH230-35816  
 ----- Summary Statistics  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 183400 bases at least Q40  
 Consensus quality: 186096 bases at least Q30  
 Consensus quality: 187794 bases at least Q20  
 Estimated insert size: 190483; sum-of-contigs estimation  
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 consists of 2 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

\* 1 255030: contig of 255030 bp in length  
 \* 255031 255130: gap of unknown length  
 \* 255131 256498: contig of 1368 bp in length.

## FEATURES

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 1. 256498  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10116"  
 /clones="CH230-35816"  
 misc\_feature  
 1. 1782  
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 clone\_end:T7"  
 2648..3813  
 /note="wgs\_end\_extension  
 clone\_end:T7"  
 misc\_feature  
 4974..7086  
 /note="wgs\_end\_extension  
 clone\_end:T7"  
 misc\_feature  
 7744..8660  
 /note="clone\_boundary  
 clone\_end:T7  
 site:MboI  
 end\_sequence:RXANT51TJB"  
 65259..66767  
 /note="wgs\_contig"  
 192091..193784  
 /note="wgs\_contig"  
 complement(252911..253807)  
 /note="clone\_boundary  
 clone\_end:Sp6  
 site:MboI  
 end\_sequence:RXANT51TVB"

## ORIGIN

Query Match 84.8%; Score 21.2; DB 2; Length 256498;  
 Best Local Similarity 72.0%; Pred. No. 7.8;  
 Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AGCCGCGCTTTCYKTRTACNAACTGCB 25  
 Db 123427 AGCGTCTTTCTTATACAACTGG 123403  
 |||||:|||||:|||||:|||||:|||||:  
 RESULT 9  
 AC121737  
 LOCUS  
 DEFINITION Rattus norvegicus clone CH230-74A9, \*\*\* SEQUENCING IN PROGRESS \*\*\*,  
 4 unordered pieces.  
 AC121737  
 VERSION AC121737.4 GI:25138094  
 HTG: HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM  
 Mammalia; Eutheria; Rodentia; Chordata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 REFERENCE  
 1 (bases 1 to 263259)  
 Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,  
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,  
 Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,  
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,  
 Bialwo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,  
 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,  
 Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,  
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,  
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,  
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 Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,  
 Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,  
 Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,  
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 Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,  
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 Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,  
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 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,  
 Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J.,  
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,  
 Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K.,  
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,  
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von  
 Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,  
 Weinstein, G. and Gibbs, R.A.

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TITLE JOURNAL
REFERENCE JOURNAL
AUTHORS JOURNAL
TITLE JOURNAL
JOURNAL
REFERENCE JOURNAL
AUTHORS JOURNAL
TITLE JOURNAL
JOURNAL
COMMENT
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GVJ
Center clone name: CH230-74A9
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 237743 bases at least Q40
Consensus quality: 237630 bases at least Q30
Consensus quality: 239718 bases at least Q20
Estimated insert size: 239635; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 257713: contig of 257713 bp in length
* 257814 257813: gap of unknown length
* 257814 258996: contig of 1183 bp in length
* 258997 259096: gap of unknown length
* 259097 261187: contig of 2091 bp in length
* 261188 261287: gap of unknown length
* 261288 263259: contig of 1972 bp in length.
Location/Qualifiers
1. 263259
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-74A9"
1. 1068
/note="wgs contig"
misc_feature
2206. 5186
/note="wgs contig"
misc_feature
256153. 257713
/note="wgs_contig"
ORIGIN

```

```

Query Match 84.8%; Score 21.2; DB 2; Length 263259;
Best Local Similarity 72.0%; Pred. No. 7.8;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTCCTTACNAACTGGB 25
|||||:|||||:|||||:|||||:
Db 156871 AGCCTGCTTTCCTTATACAACTGGG 156895

RESULT 10
AC123037 137122 bp DNA linear ROD 01-JAN-2004
LOCUS Mus musculus BAC clone RP24-527F14 from chromosome 6, complete
DEFINITION sequence.
AC123037
AC123037.4 GI:38229487
VERSION
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 137122)
Tin-Wollam,A., Cotton,M. and Boyer,E.
The sequence of Mus musculus BAC clone RP24-527F14
Unpublished (2001)
REFERENCE
2 (bases 1 to 137122)
Wilson,R.
Sequencing of Mus musculus
Unpublished (2001)
JOURNAL
3 (bases 1 to 137122)
McPherson,J.D. and Waterston,R.H.
Direct Submission
JOURNAL
Submitted (27-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 137122)
Wilson,R.K.
Direct Submission
JOURNAL
Submitted (22-OCT-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 137122)
Wilson,R.K.
Direct Submission
JOURNAL
Submitted (08-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 137122)
Wilson,R.
Direct Submission
JOURNAL
Submitted (01-JAN-2004) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 8, 2003 this sequence version replaced gi:37806531.
COMMENT
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.wustl.edu
----- Summary Statistics
Center project name: M_BB0527F14
-----

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.



**MAPPING INFORMATION:**

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

**SOURCE INFORMATION:**

The RPCI-24 BAC library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

**NEIGHBORING SEQUENCE INFORMATION:**

This sequence is the entire insert of the clone. This clone is overlapping by AC132610.

## FEATURES

source

URES	source	Location/Qualifiers
	repeat_region	1..137122 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /chromosome="6" /map="6" /clone="RP24-527P14" /clone_lib="RPC1-24" 3..340 /rpt_family="L1" 381..843 /rpt_family="L1" 847..1002 /rpt_family="L1" 2975..3194 /rpt_family="B4" 3282..3472 /rpt_family="MIR" 4605..4677 /product="tRNA-ile" 4608..4733 /rpt_family="B4" 4684..4777 /rpt_family="7SLRNA" 7022..7169 /rpt_family="Alu" 7205..7545 /rpt_family="MaLR" 7947..8108 /rpt_family="B2" 8109..9238 /rpt_family="L1" 9951..10110 /rpt_family="MaLR" 10893..11256 /rpt_family="MaLR" 11321..11682 /rpt_family="MaLR" 11832..12502 /rpt_family="L1" 13014..13150 /rpt_family="ERV1" 13195..13588 /rpt_family="ERV1" 20736..21052 /rpt_family="L1" 22934..22994 /rpt_family="ERV1" 22980..23035 /rpt_family="ERV1" 23707..23887 /rpt_family="B2" 23909..24338 /rpt_family="L1" 24352..24428 /rpt_family="L1" 24891..25446 repeat_region

Db 86972 AGCGTGCTTCTTATACAACTGG 86995

RESULT 11  
AC147382  
LOCUS AC147382 198872 bp DNA linear PRI 19-MAY-2004  
DEFINITION Pan troglodytes BAC clone RP43-171M24 from 7, complete sequence.  
ACCESSION AC147382  
VERSION AC147382.3 GI:45736892  
KEYWORDS HTG.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
TITLE 1 (bases 1 to 198872)  
JOURNAL The sequence of Pan troglodytes BAC clone RP43-171M24  
AUTHORS Shah, N., Bielicki, L. and Haglund, K.  
REFERENCE 2 (bases 1 to 198872)  
AUTHORS Unpublished (2001)  
TITLE Wilson, R.K.  
JOURNAL Direct Submission  
REFERENCE 3 (bases 1 to 198872)  
AUTHORS Submitted (11-NOV-2003) Genetics, Genome Sequencing Center, 4444  
TITLE Forest Park Parkway, St. Louis, MO 63108, USA  
JOURNAL Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (25-FEB-2004) Genetics, Genome Sequencing Center, 4444  
AUTHORS Forest Park Parkway, St. Louis, MO 63108, USA  
TITLE 4 (bases 1 to 198872)  
JOURNAL Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (19-MAY-2004) Washington University School of Medicine,  
AUTHORS Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO  
TITLE 5 (bases 1 to 198872)  
JOURNAL Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On Mar 25, 2004 this sequence version replaced gi:42734583.  
----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu>  
Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)  
----- Summary Statistics -----  
Center project name: C\_PT171M24  
-----

NOTICE:  
This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by sequence  
from more than one subclone; and the assembly was confirmed by  
restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. Wes Warren,  
Department of Genetics, Washington University, St. Louis MO. For  
additional information about the map position of this sequence, see  
<http://genome.wustl.edu>

SOURCE INFORMATION:  
The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA  
was isolated from white blood cells obtained from a male chimpanzee  
(Pan troglodytes, 'Clint', Yerkes #C0471, birthdate: 6-6-80). The  
clone and detailed information can be obtained from ResGen  
(<http://www.resgen.com>) or Pieter de Jong and co-workers at  
<http://www.bacpac.chori.org>.

NEIGHBORING SEQUENCE INFORMATION:  
This sequence is the entire insert of the clone. This clone is  
overlapped by AC146098.

FEATURES  
source  
Location/Qualifiers  
1..198872  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/chromosome="7"  
/map="7"  
/clone="RP43-171M24"  
/clone\_lib="RPCI-43"

ORIGIN  
Query Match 84.0%; Score 21; DB 9; Length 198872;  
Best Local Similarity 75.0%; Pred. No. 10;  
Matches 18; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 AGCCGCTTTTCTTATACAACTSG 24  
|||||:|||||:|||||:|||||  
Db 63546 AGCCAGCTTTGTATACCACTGG 63569

RESULT 12  
AC125159/c  
LOCUS AC125159 204431 bp DNA linear HTG 25-AUG-2002  
DEFINITION Mus musculus chromosome UNK clone RP24-394C23, WORKING DRAFT  
SEQUENCE, 8 unordered pieces.  
AC125159  
AC125159.3 GI:22476252  
HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_FULLTOP.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 204431)  
AUTHORS McPherson, J.D. and Waterston, R.H.  
TITLE The sequence of Mus musculus clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 204431)  
AUTHORS McPherson, J.D. and Waterston, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA  
REFERENCE 3 (bases 1 to 204431)  
AUTHORS McPherson, J.D. and Waterston, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA  
COMMENT On Aug 25, 2002 this sequence version replaced gi:22002221.  
----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc/index.shtml>  
Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)  
----- Project Information -----  
Center project name: M\_BB0394C23  
-----

----- Summary Statistics -----  
Sequencing vector: M13; 0%  
Sequencing vector: plasmid; 100%  
Chemistry: Dye-primer ET; 0% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 201646 bases at least Q40  
Consensus quality: 202298 bases at least Q30  
Consensus quality: 202670 bases at least Q20  
Insert size: 139000; agarose-fp  
Insert size: 203731; sum-of-contigs  
Quality coverage: 13.99 in Q20 bases; agarose-fp  
Quality coverage: 11.84 in Q20 bases; sum-of-contigs  
-----

\* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 3397: contig of 3397 bp in length  
3398 3497: gap of unknown length  
3498 11345: contig of 7848 bp in length  
11346 11445: gap of unknown length  
11446 33842: contig of 22397 bp in length  
33843 33942: gap of unknown length  
33943 63612: contig of 29670 bp in length  
63613 63712: gap of unknown length  
63713 91001: contig of 27289 bp in length  
91002 91101: gap of unknown length  
91102 123616: contig of 32515 bp in length  
123617 123716: gap of unknown length  
123717 162626: contig of 38910 bp in length  
162627 162726: gap of unknown length  
162727 204431: contig of 41705 bp in length.

FEATURES  
source

1..204431  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/chromosome="UNK"  
/clone="RP24-394C23"  
1..3397  
/note="assembly\_name:Contig12"  
3498..11345  
/note="assembly\_name:Contig13"  
11446..33842  
/note="assembly\_name:Contig14"  
33943..63612  
/note="assembly\_name:Contig15"  
63713..91001  
/note="assembly\_name:Contig16"  
91102..123616  
/note="assembly\_name:Contig17"  
123717..162626  
/note="assembly\_name:Contig18"  
162727..204431  
/note="assembly\_name:Contig19"

ORIGIN

Query Match 84.0%; Score 21; DB 2; Length 204431;  
Best Local Similarity 75.0%; Pred. No. 10;  
Matches 18; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTCTTACNACTSG 24

Db 56693 AGCCTGCTTTCTTATACAACTGG 56670

RESULT 13

BD131366 BD131366 25 bp DNA linear PAT 18-SEP-2002  
LOCUS Recombinational cloning using nucleic acids having recombination sites.

ACCESSION BD131366  
VERSION BD131366.1 GI:23226311  
KEYWORDS JP 2002500861-A/40.  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.  
TITLE Recombinational cloning using nucleic acids having recombination sites  
JOURNAL Patent: JP 2002500861-A 40 15-JAN-2002;  
LIFE TECHNOLOGIES INC

COMMENT OS Unknown  
PN JP 2002500861-A/40  
PD 15-JAN-2002  
PF 26-OCT-1998 JP 2000518069  
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI  
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC  
C12N15/09, C12Q1/68, C12N15/00  
CC Description of Unknown Organism: recombination products FH  
Key source Location/Qualifiers  
FT source 1..25  
/organism="Unknown".

FEATURES  
source

1..25  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 81.6%; Score 20.4; DB 6; Length 25;  
Best Local Similarity 76.0%; Pred. No. 30;  
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTCTTACNACTSG 25

Db 1 ASCCGCTTTTCTTACAACTG 25

RESULT 14

AR124526 AR124526 25 bp DNA linear PAT 16-MAY-2001  
LOCUS Sequence 6 from patent US 6171861.  
DEFINITION AR124526  
ACCESSION AR124526  
VERSION AR124526.1 GI:14109887  
KEYWORDS  
SOURCE Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 25)

AUTHORS Hartley, J.L. and Brasch, M.A.

TITLE Recombinational cloning using engineered recombination sites

JOURNAL Patent: US 6171861-A 6 09-JAN-2001;

FEATURES  
source

1..25  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 80.0%; Score 20; DB 6; Length 25;  
Best Local Similarity 72.0%; Pred. No. 48;  
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTCTTACNACTSG 25

Db 1 AGCCTGCTTTTCTTACAACTGT 25

RESULT 15

AR124527 AR124527 25 bp DNA linear PAT 16-MAY-2001  
LOCUS Sequence 7 from patent US 6171861.  
DEFINITION AR124527  
ACCESSION AR124527  
VERSION AR124527.1 GI:14109888  
KEYWORDS  
SOURCE Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 25)

AUTHORS Hartley, J.L. and Brasch, M.A.

TITLE Recombinational cloning using engineered recombination sites

JOURNAL Patent: US 6171861-A 7 09-JAN-2001;

FEATURES  
source

1..25  
/organism="unknown"

ORIGIN /mol\_type="unassigned DNA"  
Query Match 80.0%; Score 20; DB 6; Length 25;  
Best Local Similarity 72.0%; Pred. No. 48;  
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGCCWGCCTTYKRTACNAACTSGE 25  
|||:|||||:|:|:|:|:|:|:|:|:|:  
Db 1 AGCCTGCTTCTTGTACAAACTGT 25

Search completed: November 16, 2004, 06:00:59  
Job time : 710.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds  
(without alignments)  
782.095 Million cell updates/sec

Title: US-10-820-133-2

Perfect score: 25

Sequence: 1 agcgwgttkttracnaactsqb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134896 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_23Sep04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.2	84.8	25	2	AAT48211
2	21.2	84.8	25	2	AAX78936
3	21.2	84.8	25	4	AAC87867
4	21.2	84.8	25	4	AAT55736
5	21.2	84.8	25	4	AAD14430
6	21.2	84.8	25	8	ABT16622
7	21.2	84.8	25	9	ACD28277
8	21.2	84.8	25	9	ACD28477
9	21.2	84.8	25	9	ADA38163
10	21.2	84.8	25	10	AAD60559
11	21.2	84.8	25	10	ACC44651
12	21.2	84.8	25	12	ADL93417
13	20.4	81.6	25	2	AAX78974
14	20	80.0	25	2	AAT48216
15	20	80.0	25	2	AAT48215
16	20	80.0	25	2	AAX78940
17	20	80.0	25	2	AAX78941
18	20	80.0	25	3	AAX55380
19	20	80.0	25	4	AAS06178
c 20	20	80.0	25	4	AAC87899
c 21	20	80.0	25	4	AAC87898

22	20	80.0	25	4	AAC87872	Aac87872 Escherich
23	20	80.0	25	4	AAC87871	Aac87871 Escherich
24	20	80.0	25	4	AAF55740	Aaf55740 Recombina
c 25	20	80.0	25	4	AAF55767	Aaf55767 PCR prime
c 26	20	80.0	25	4	AAF55768	Aaf55768 PCR prime
c 27	20	80.0	25	4	AAF55741	Aaf55741 Recombina
c 28	20	80.0	25	4	AAH22542	Aah22542 ATT site
29	20	80.0	25	4	AAH22542	Aah22542 ATT site
30	20	80.0	25	4	AAH22542	Aah22542 ATT site
31	20	80.0	25	6	ABQ82118	Abq82118 Core sequ
32	20	80.0	25	6	ABQ82119	Abq82119 Core sequ
33	20	80.0	25	8	ABT16626	Abt16626 Artificia
c 34	20	80.0	25	9	ACD28428	Acd28428 Engineere
35	20	80.0	25	9	ACD28281	Acd28281 Nucleic a
36	20	80.0	25	9	ACD28282	Acd28282 Nucleic a
c 37	20	80.0	25	9	ACD28429	Acd28429 Engineere
38	20	80.0	25	9	ACD28481	Acd28481 Nucleic a
39	20	80.0	25	9	ACD28482	Acd28482 Nucleic a
c 40	20	80.0	25	9	ACD28607	Acd28607 Engineere
c 41	20	80.0	25	9	ACD28608	Acd28608 Engineere
c 42	20	80.0	25	9	ADA38195	Ada38195 Complemen
c 43	20	80.0	25	9	ADA38194	Ada38194 Complemen
44	20	80.0	25	9	ADA38167	Ada38167 DNA of a
45	20	80.0	25	9	ADA38168	Ada38168 DNA of a

ALIGNMENTS

RESULT 1

AAT48211  
ID AAT48211 standard; DNA; 25 BP.

AC AAT48211;

DT 20-OCT-1997 (first entry)

DE M-attB core region.

XX att recombination site; core region; mutation; enhance; recombination;  
vector; subcloning; regulation; exchange; ss.

OS Synthetic.

PN WO9640724-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US010082.

PR 07-JUN-1995; 95US-00486139.

PA (LIFE-) LIFE TECHNOLOGIES INC.

PI Hartley JL, Brasch MA;

DR WPI; 1997-065168/06.

PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
using recombinant proteins and engineered recombination sites in vitro or  
in vivo.

PS Claim 14; Page 55; 106pp; English.

CC AAT48210-25 are att recombination site core region DNA sequences. The  
core region has at least one engineered mutation that enhances  
recombination in vitro in the formation of a Cointegrate or Product DNA.  
These core regions can be incorporated into novel vector donor DNA  
molecules. The nucleic acids, vectors and methods of the invention are  
used to obtain chimeric nucleic acid using recombination proteins and  
engineered recombination sites in vitro or in vivo. The improved  
specificity, speed and yields of the invention facilitates DNA or RNA  
subcloning, regulation or exchange useful for any related purpose, e.g.

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
CC or modification of transcribed, replicated, isolated or genomic DNA or  
CC RNA

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 84.8%; Score 21.2; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCGCTTYYKTRTACNAACTSGB 25  
Db 1 AGCCGCGCTTYYKTRTACNAACTSGB 25

## RESULT 2

AAAX78936

ID AAX78936 standard; DNA; 25 BP.

AC AAX78936;

XX 17-AUG-1999 (first entry)

DT DT

XX Oligonucleotide #2 for recombination and cloning method.

DE Cloning; donor; recombination site; vector; chimeric; ss.

XX Synthetic.

OS WO9921977-A1.

XX 06-MAY-1999.

PN 26-OCT-1998; 98WO-US022589.

XX 24-OCT-1997; 97US-0065930P.

XX 23-OCT-1998; 98US-00177387.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Fox DK;

XX WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

XX Disclosure; Page 159; 185pp; English.

CC The invention relates to novel methods for cloning or subcloning one or  
CC more nucleic acid molecules (NAMS) comprising: (a) combining in vitro or  
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
CC more desired nucleic acid segments flanked by at least 2 recombination  
CC sites which do not recombine with each other; (2) one or more vector  
CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
CC not recombine with each other; and (3) one or more site-specific  
CC recombination proteins; (b) incubating the combination to transfer one or  
CC more of the desired segments into one or more of the VDMs, thereby  
CC producing one or more desired product molecules (PMs). The methods can be  
CC used for the efficient and specific recombination of NAM segments. They  
CC can be used to generate chimeric DNA or RNA molecules that have the  
CC desired characteristics and/or nucleic acid segments. The methods can  
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
CC are used in the method of the invention

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 84.8%; Score 21.2; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCGCTTYYKTRTACNAACTSGB 25  
Db 1 AGCCGCGCTTYYKTRTACNAACTSGB 25

## RESULT 3

AAC87867

ID AAC87867 standard; DNA; 25 BP.

XX AAC87867;

XX 02-MAR-2001 (first entry)

DT DT

XX Escherichia coli core region recombinant site m-attB SEQ ID NO:2.

DE Core region; recombination site; cloning; chimeric DNA; characteristic;  
XX mutation; att site; lox site; ss.

XX Escherichia coli.

OS US6143557-A.

XX 07-NOV-2000.

PN 20-JAN-1999; 99US-00233493.

XX 07-JUN-1995; 95US-00486139.

XX 07-JUN-1996; 96US-00663002.

XX 12-JAN-1998; 98US-00005476.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Brasch MA, Hartley JL;

XX WPI; 2001-049004/06.

PT Isolated nucleic acid molecules comprising a DNA segment having two  
PT engineered recombination sites, derived from att or lox, which flank a  
PT selectable marker and comprise a core region having an engineered  
PT mutation.

XX Claim 1; Col 18; 73pp; English.

CC The present invention describes an isolated nucleic acid molecule (I)  
CC comprising a first nucleic acid sequence having a defined sequence  
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,  
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described  
CC are: (1) an isolated nucleic acid molecule (II) comprising a first  
CC mutated recombination site that removes one or more stop codons from the  
CC recombination site or avoids hairpin formation, the recombination site  
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)  
CC comprising a first att recombination site comprising a mutation that  
CC enhances recombination specificity; (3) vectors (IV) comprising the above  
CC mentioned nucleic acids; and (4) cells comprising the above mentioned  
CC nucleic acids or (IV). The nucleic acids are used in engineering a core  
CC region of a given recombination site to provide mutative sites suitable  
CC for subcloning reactions. The use of nucleic acids for obtaining  
CC engineered recombination in vitro or in vivo makes the methods for DNA or  
CC RNA subcloning, highly specific, rapid, and less labour intensive

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 84.8%; Score 21.2; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCGCTTYYKTRTACNAACTSGB 25  
Db 1 AGCCGCGCTTYYKTRTACNAACTSGB 25

## RESULT 4

AAF55736

ID AAF55736 standard; DNA; 25 BP.

XX AAF55736;

```
XX 12-APR-2001 (first entry)
XX DT
XX DE
XX REcombination site m-attB.
XX KW
XX OS
XX Unidentified.
XX PN
XX US6171861-B1.
XX PD
XX 09-JAN-2001.
XX PF
XX 12-JAN-1998; 98US-00005476.
XX PR
XX 07-JUN-1995; 95US-00486139.
XX PR
XX 07-JUN-1996; 96US-00663002.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX PA
XX Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX
XX In vitro cloning of nucleic acid involves mixing vectors comprising
XX recombination sites and/or nucleic acid, incubating mixture to produce
XX chimeric molecule, contacting hosts with mixture and selecting host.
XX
XX Claim 24; Col 46; 73pp; English.
XX
XX The present invention relates to a method for in vitro cloning of a
XX nucleic acid of interest. The method involves mixing in vitro two vectors
XX each comprising at least one recombination site and the nucleic acid of
XX interest; incubating the mixture in the presence of at least one
XX recombination protein to result in recombination of the recombination
XX sites, leading to production of a chimeric nucleic acid molecule
XX comprising the nucleic acid of interest; contacting hosts with the
XX mixture; and selecting for a host comprising the chimeric nucleic acid
XX molecule, and selecting against a host comprising the vectors comprising
XX the second vector, to clone the nucleic acid. The present sequence is a
XX recombination site, which may be used in the method of the present
XX invention
XX
XX Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;
XX
Query Match 84.8%; Score 21.2; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCCGCTTTTKRTACNAACTSGB 25
Db 1 AGCCGCTTTTKRTACNAACTSGB 25
RESULT 5
AADI4430
ID AADI4430 standard; DNA; 25 BP.
XX
XX AADI4430;
XX
XX 01-NOV-2001 (first entry)
XX DT
XX DE
XX Recombination site m-attB DNA.
XX
XX Recombination site; copy number; replicon; recombinatorial cloning;
XX m-attB; ds.
XX
XX Unidentified.
XX OS
XX US6270969-B1.
XX PN
XX 07-AUG-2001.
XX PD
XX
XX 12-APR-2001 (first entry)
XX DT
XX DE
XX Recombination site m-attB.
XX KW
XX OS
XX Unidentified.
XX PN
XX US6171861-B1.
XX PD
XX 09-JAN-2001.
XX PF
XX 12-JAN-1998; 98US-00005476.
XX PR
XX 07-JUN-1995; 95US-00486139.
XX PR
XX 07-JUN-1996; 96US-00663002.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX PA
XX Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX
XX In vitro cloning of nucleic acid involves mixing vectors comprising
XX recombination sites and/or nucleic acid, incubating mixture to produce
XX chimeric molecule, contacting hosts with mixture and selecting host.
XX
XX Claim 24; Col 46; 73pp; English.
XX
XX The present invention relates to a method for in vitro cloning of a
XX nucleic acid of interest. The method involves mixing in vitro two vectors
XX each comprising at least one recombination site and the nucleic acid of
XX interest; incubating the mixture in the presence of at least one
XX recombination protein to result in recombination of the recombination
XX sites, leading to production of a chimeric nucleic acid molecule
XX comprising the nucleic acid of interest; contacting hosts with the
XX mixture; and selecting for a host comprising the chimeric nucleic acid
XX molecule, and selecting against a host comprising the vectors comprising
XX the second vector, to clone the nucleic acid. The present sequence is a
XX recombination site, which may be used in the method of the present
XX invention
XX
XX Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;
XX
Query Match 84.8%; Score 21.2; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCCGCTTTTKRTACNAACTSGB 25
Db 1 AGCCGCTTTTKRTACNAACTSGB 25
RESULT 6
ABT16622
ID ABT16622 standard; DNA; 25 BP.
XX
XX ABT16622;
XX
XX 03-APR-2003 (first entry)
XX DT
XX DE
XX Artificial plant chromosome related oligo SEQ ID No 34.
XX
XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
XX blood factor; herbicide; stress; agronomical; nutrient quality;
XX bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
XX ds.
XX
XX Unidentified.
XX OS
XX WO200296923-A1.
XX PN
XX 05-DEC-2002.
XX PD
XX 30-MAY-2002; 2002WO-US017451.
XX PF
XX 30-MAY-2001; 2001US-0294687P.
XX PR
XX 04-JUN-2001; 2001US-0296329P.
XX PR
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX PA
XX (AGRI-) AGRISOMA INC.
XX
```

PI Perez C, Fabijanski SF, Perkins E;  
 XX WPI; 2003-140436/13.  
 XX  
 PT Producing artificial chromosome by introducing a nucleic acid into plant  
 PT cell, selecting artificial chromosome that has one or more repeat regions  
 PT with equivalent amounts of euchromatic and heterochromatic nucleic acids.  
 XX  
 XX Disclosure; Page 261; 269pp; English.  
 XX  
 CC The invention relates to a novel method for producing plant artificial  
 CC chromosomes. The invention also relates to methods for targeting  
 CC insertion of heterologous DNA into plant artificial chromosomes, methods  
 CC for delivery of plant chromosomes to selected cells and tissues. The  
 CC isolated plant artificial chromosome (PAC) is useful for producing a  
 CC transgenic plant, which involves introducing the PAC into a plant cell.  
 CC The PAC comprises a heterologous nucleic acid encoding a gene product  
 CC such as enzymes, antisense RNA, rDNA, structural proteins, marker  
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and  
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,  
 CC cytokines, growth factors, antibodies, or a product that provides for  
 CC resistance to diseases, insects, herbicides, or stress in a plant. The  
 CC heterologous nucleic acid optionally encodes a product that provides an  
 CC agronomically important trait in the plant, e.g. a product that alters  
 CC nutrient use and/or improves the nutrient quality of the plant. The  
 CC heterologous nucleic acid is contained within a bacterial artificial  
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This  
 CC polynucleotide sequence represents an oligo relating to the method for  
 CC producing plant artificial chromosomes of the invention  
 XX  
 SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;  
 Query Match 84.8%; Score 21.2; DB 8; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCCGCTTYYKTRTACNAACTSG 25  
 Db 1 AGCCGCTTYYKTRTACNAACTSG 25  
 |||||  
 |||||  
 RESULT 7  
 ACD28277  
 ID ACD28277 standard; DNA; 25 BP.  
 XX  
 AC ACD28277;  
 XX  
 DT 02-OCT-2003 (first entry)  
 XX  
 DE Nucleic acid core region m-attB.  
 XX  
 KW Core region; ds; vector donor DNA; flanking recombination site; m-attB.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003064515-A1.  
 XX  
 PD 03-APR-2003.  
 XX  
 PF 30-JAN-2002; 2002US-00058291.  
 XX  
 PR 07-JUN-1995; 95US-00486139.  
 PR 07-JUN-1996; 96US-00663002.  
 PR 20-JAN-1999; 99US-00233493.  
 PR 02-NOV-1999; 99US-00432085.  
 XX  
 PA (HARTLEY) HARTLEY J L.  
 PA (BRASCH) BRASCH M A.  
 XX  
 PI Hartley JL, Brasch MA;  
 XX  
 DR WPI; 2003-540791/51.  
 XX

PT New Vector Donor DNA molecule for recombinational cloning using  
 PT engineered recombination sites, comprises first and second DNA segments  
 PT that do not recombine with each other and that contain a Selectable  
 PT marker.  
 XX  
 XX Claim 14; Page 25; 71pp; English.  
 XX  
 CC The invention relates to a vector donor DNA molecule comprising a first  
 CC DNA segment and a second DNA segment containing at least one selectable  
 CC marker. The first and second segments are separated either by, in a  
 CC circular vector donor, a first and a second recombination site, or in a  
 CC linear vector donor, at least a first recombination site, where each pair  
 CC of flanking recombination sites are engineered and do not recombine with  
 CC each other. The nucleic acid molecule, vectors and methods are useful for  
 CC moving or exchanging segments of DNA molecules using engineered  
 CC recombination sites and recombination proteins to provide chimeric DNA  
 CC molecules that have the desired characteristic(s) and/or DNA segment(s).  
 CC The present sequence represents the nucleic acid core region m-attB  
 XX  
 SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;  
 Query Match 84.8%; Score 21.2; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCCGCTTYYKTRTACNAACTSG 25  
 Db 1 AGCCGCTTYYKTRTACNAACTSG 25  
 |||||  
 |||||  
 RESULT 8  
 ACD28477  
 ID ACD28477 standard; DNA; 25 BP.  
 XX  
 AC ACD28477;  
 XX  
 DT 09-OCT-2003 (first entry)  
 XX  
 DE Nucleic acid core sequence m-attB.  
 XX  
 KW Nucleic acid core; m-attB; cointegrate DNA; flanking recombination site;  
 KW ds.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003068799-A1.  
 XX  
 PD 10-APR-2003.  
 XX  
 PF 06-JUN-2002; 2002US-00162879.  
 XX  
 PR 07-JUN-1995; 95US-00486139.  
 PR 07-JUN-1996; 96US-00663002.  
 PR 20-JAN-1999; 99US-00233493.  
 PR 02-NOV-1999; 99US-00432085.  
 XX  
 PA (INVI-) INVITROGEN CORP.  
 XX  
 PI Hartley JL, Brasch MA;  
 XX  
 DR WPI; 2003-540884/51.  
 XX  
 CC Making CoIntegrate DNA molecule, by combining recombination sites  
 CC flanking the desired DNA segment in insert donor DNA, with the  
 CC recombination sites of vector donor DNA, using site specific  
 CC recombination protein.  
 XX  
 XX Claim 14; Page 25; 71pp; English.  
 XX  
 CC The invention relates to a method of making a coIntegrate DNA molecule.  
 CC The method is useful for making a coIntegrate DNA molecule. The method is  
 CC useful for a variety of DNA exchanges, such as subcloning of DNA, in  
 CC vitro or in vivo. The method enables efficient and specific recombination



CC of DNA segments using recombination proteins. The method is highly  
 CC specific, rapid and less labour intensive. The improved specificity,  
 CC yield and speed of the method facilitates DNA or RNA subcloning,  
 CC regulation and exchange useful for other related purposes. Since single  
 CC molecules of the recombinations product can be introduced into a  
 CC biological host, propagation of the desired product DNA in the absence of  
 CC other DNA molecules is more readily realised. Reaction conditions can be  
 CC freely adjusted in vitro to optimise enzyme activities. The present  
 CC sequence represents the nucleic acid core sequence m-attB  
 CC  
 SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;  
 Query Match 84.8%; Score 21.2; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCCGCTTTTKRTACNAACTSG 25  
 DB 1 AGCCGCTTTTKRTACNAACTSG 25  
 RESULT 9  
 ADA38163  
 ID ADA38163 standard; DNA; 25 BP.  
 XX  
 AC ADA38163;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE m-attB DNA sequence indicating generic core region of an attB site.  
 XX  
 KW engineered recombination site; cloning; recombinase; subcloning; attB;  
 KW attP; attL; attR; selectable marker; cointegrate; m-attB; ds.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003054552-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 30-JAN-2002; 2002US-00058292.  
 XX  
 PR 07-JUN-1995; 95US-00486139.  
 PR 07-JUN-1996; 96US-00663002.  
 PR 20-JAN-1999; 99US-00233493.  
 PR 02-NOV-1999; 99US-00432085.  
 XX  
 PA (HARTLEY) HARTLEY J L.  
 PA (BRAS) BRASCH M A.  
 XX  
 PI Hartley JL, Brasch MA;  
 XX  
 DR WPI; 2003-585168/55.  
 XX  
 PT New Vector Donor DNA molecule, useful for recombinational cloning  
 PT purposes, comprises a first and a second DNA segment that contains a  
 PT selectable marker and is separated by a pair of flanking, engineered  
 PT recombination sites.  
 XX  
 PS Claim 14; Page 26; 72pp; English.  
 XX  
 CC This invention relates to novel DNA and vectors having engineered  
 CC recombination sites for use in a cloning method that enables efficient  
 CC and specific recombination of DNA segments using recombination proteins  
 CC including recombinases. As such, it provides a method for obtaining  
 CC chimeric nucleic acids with the desired characteristics, facilitating DNA  
 CC or RNA subcloning, regulation and/or exchange. The recombination site is  
 CC derived from attB attP, attL or attR, where the att site is att1, att2 or  
 CC att3. Engineered mutations of the att sites (either one or multiple  
 CC mutations) can enhance specificity or efficiency of the recombination  
 CC reaction and the properties of the product DNA molecules. Accordingly,  
 CC the present invention describes a nucleic acid molecule comprising at  
 CC least one DNA segment having at least two engineered recombination sites

CC flanking a selectable marker and/or a desired DNA segment. Furthermore,  
 CC at least one of the engineered sites must enhance recombination in vitro  
 CC to form a cointegrate or product DNA molecule. This oligonucleotide  
 CC sequence is m-attB, a generic DNA sequence indicating the core region of  
 CC an attB recombination site of the invention.  
 XX  
 SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;  
 Query Match 84.8%; Score 21.2; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCCGCTTTTKRTACNAACTSG 25  
 DB 1 AGCCGCTTTTKRTACNAACTSG 25  
 RESULT 10  
 AAD60559  
 ID AAD60559 standard; DNA; 25 BP.  
 XX  
 AC AAD60559;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Core region DNA, m-attB.  
 XX  
 KW Recombinational cloning; DNA exchange; core region; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003100110-A1.  
 XX  
 PD 29-MAY-2003.  
 XX  
 PF 02-NOV-1999; 99US-00432085.  
 XX  
 PR 07-JUN-1995; 95US-00486139.  
 PR 07-JUN-1996; 96US-00663002.  
 PR 20-JAN-1999; 99US-00233493.  
 XX  
 PA (HARTLEY) HARTLEY J L.  
 PA (BRAS) BRASCH M A.  
 XX  
 PI Hartley JL, Brasch MA;  
 XX  
 DR WPI; 2003-730143/69.  
 XX  
 PT New Vector Donor DNA molecule for recombinational cloning using  
 PT engineered recombination sites, comprises first and second DNA segments  
 PT that do not recombine with each other and that contain a selectable  
 PT marker.  
 XX  
 PS Claim 14; Page 25; 71pp; English.  
 XX  
 CC The invention relates to a vector donor DNA molecule which comprises  
 CC first and second DNA segments that do not recombine with each other and  
 CC that contain a selectable marker. The invention also relates to a method  
 CC for recombinational cloning using engineered recombination sites. The  
 CC invention is useful for moving or exchanging segments of DNA molecules  
 CC using engineered recombination sites and recombination proteins to  
 CC provide chimeric DNA molecules that have the desired characteristic(s)  
 CC and/or DNA segment(s). The present sequence is a core region DNA. This  
 CC sequence is used to illustrate the method of the invention  
 XX  
 SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;  
 Query Match 84.8%; Score 21.2; DB 10; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCCGCTTTTKRTACNAACTSG 25

```
Db      1  AGCCWGCCTTYYKTRTACNACTSGB 25

RESULT 11
ACC44651
ID  ACC44651 standard; DNA; 25 BP.
XX
AC  ACC44651;
XX
XX
DT  29-MAY-2003  (first entry)
XX
DE  Recombination site related oligonucleotide SEQ ID NO:42.
XX
XX  Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
KW  att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
KW  platform artificial chromosome expression system; PCR primer; ss.
XX
OS  Synthetic.
XX
XX  WO200297059-A2.
PN
XX
XX  05-DEC-2002.
PD
XX
XX  30-MAY-2002; 2002WO-US017452.
PF
XX
XX  30-MAY-2001; 2001US-0294758P.
PR
XX  21-MAR-2002; 2002US-0366891P.
PR
XX
XX  (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
PA
XX
XX  Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
PI  Stewart S, Shellard J;
PI
XX
XX  WPI; 2003-140461/13.
DR
XX
XX  Novel eukaryotic chromosome comprising one or many att sites which
PT  permits site-directed integration in the presence of lambda-integrase,
PT  useful for site-specific recombination-directed integration of DNA of
PT  interest.
XX
XX  Claim 43; Page 143; 272pp; English.
PS
XX
XX  The present invention describes a eukaryotic chromosome (I) comprising
CC  one or several att sites, where an att site is heterologous to the
CC  chromosome, and permits site-directed integration in the presence of
CC  lambda-integrase. Also described: (1) a platform artificial chromosome
CC  expression system (ACes) (II) comprising several sites that participate
CC  in recombinase catalysed recombination; and (2) a method (M1) for
CC  introducing a heterologous nucleic acid into a platform artificial
CC  chromosome. (I) can be used in gene therapy. (M1) is useful for
CC  introducing a heterologous nucleic acid molecule into a platform
CC  artificial chromosome, preferably an ACes. (II) is useful for producing a
CC  transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
CC  mammal) by introducing (II) by cell fusion, lipid-mediated transfection
CC  by a carrier system, microinjection, microcell fusion, electroporation,
CC  microprojectile bombardment or direct DNA transfer into an embryonic
CC  cell, preferably a stem cell or an embryo. (II) comprises a heterologous
CC  nucleic acid that encodes a therapeutic product which is useful for
CC  making a library of ACes comprising random portions of a genome. ACC44612
CC  to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
CC  exemplification of the present invention
XX
XX  Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;
SQ
Query Match      84.8%; Score 21.2; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  AGCCWGCCTTYYKTRTACNACTSGB 25
|||||
Db      1  AGCCWGCCTTYYKTRTACNACTSGB 25
```

Qy 1 AGCCGCTTYYKTRTACNAACTSG 25  
 Db 1 AGCCGCTTYYKTRTACNAACTSG 25

RESULT 13  
 AAX78974  
 ID AAX78974 standard; DNA; 25 BP.  
 XX AC AAX78974;  
 XX DT 17-AUG-1999 (first entry)  
 XX DE Oligonucleotide #40 for recombination and cloning method.  
 XX KW Cloning; donor; recombination site; vector; chimeric; ss.  
 XX OS Synthetic.  
 XX PN WO9921977-A1.  
 XX PD 06-MAY-1999.  
 XX PF 26-OCT-1998; 98WO-US022589.  
 XX PR 24-OCT-1997; 97US-0065930P.  
 XX PR 23-OCT-1998; 98US-00177387.  
 XX PA (LIFE-) LIFE TECHNOLOGIES INC.  
 XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;  
 XX DR WPI; 1999-303011/25.  
 XX PT New nucleic acid cloning methods.  
 XX PS Disclosure; Page 170; 185pp; English.

CC The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAs) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecule (IDMs) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMs) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more site-specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMs, thereby producing one or more desired product molecules (PMs). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention

XX SQ Sequence 25 BP; 4 A; 4 C; 2 G; 7 T; 0 U; 8 Other;  
 Query Match 81.6%; Score 20.4; DB 2; Length 25;  
 Best Local Similarity 76.0%; Pred. No. 4.7;  
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTACNAACTSG 25  
 Db 1 ASCCGCTTYYKTRTACNAASTKG 25

RESULT 14  
 AAT48216  
 ID AAT48216 standard; DNA; 25 BP.  
 XX AC AAT48216;  
 XX DT 20-OCT-1997 (first entry)

CC The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAs) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecule (IDMs) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMs) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more site-specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMs, thereby producing one or more desired product molecules (PMs). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention

XX SQ Sequence 25 BP; 4 A; 4 C; 2 G; 7 T; 0 U; 8 Other;  
 Query Match 81.6%; Score 20.4; DB 2; Length 25;  
 Best Local Similarity 76.0%; Pred. No. 4.7;  
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

XX attB2 core region.  
 DE att recombination site; core region; mutation; enhance; recombination;  
 KW vector; subcloning; regulation; exchange; ss.  
 XX OS Synthetic.  
 XX PN WO9640724-A1.  
 XX PD 19-DEC-1996.  
 XX PF 07-JUN-1996; 96WO-US010082.  
 XX PR 07-JUN-1995; 95US-00486139.  
 XX PA (LIFE-) LIFE TECHNOLOGIES INC.  
 XX PI Hartley JL, Brasch MA;  
 XX DR WPI; 1997-065168/06.  
 XX PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid - using recombinant proteins and engineered recombination sites in vitro or in vivo.  
 XX PS Claim 14; Page 55; 106pp; English.

CC AAT48210-25 are att recombination site core region DNA sequences. The core region has at least one engineered mutation that enhances recombination in vitro in the formation of a Cointegrate or Product DNA. These core regions can be incorporated into novel vector donor DNA molecules. The nucleic acids, vectors and methods of the invention are used to obtain chimeric nucleic acid using recombination proteins and engineered recombination sites in vitro or in vivo. The improved specificity, speed and yields of the invention facilitates DNA or RNA subcloning, regulation or exchange useful for any related purpose, e.g. in vitro recombination of DNA segments, and in vitro or in vivo insertion or modification of transcribed, replicated, isolated or genomic DNA or RNA

XX SQ Sequence 25 BP; 5 A; 6 C; 4 G; 10 T; 0 U; 0 Other;  
 Query Match 80.0%; Score 20; DB 2; Length 25;  
 Best Local Similarity 72.0%; Pred. No. 7.4;  
 Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTACNAACTSG 25  
 Db 1 AGCCTGCTTCTTGTCACAACTTGT 25

RESULT 15  
 AAT48215  
 ID AAT48215 standard; DNA; 25 BP.  
 XX AC AAT48215;  
 XX DT 20-OCT-1997 (first entry)  
 XX DE attB1 core region.  
 XX KW att recombination site; core region; mutation; enhance; recombination;  
 XX KW vector; subcloning; regulation; exchange; ss.  
 XX OS Synthetic.  
 XX PN WO9640724-A1.  
 XX PD 19-DEC-1996.  
 XX PF 07-JUN-1996; 96WO-US010082.  
 XX DT

PR 07-JUN-1995; 95US-00486139.  
XX  
XX (LIFE-) LIFE TECHNOLOGIES INC.  
XX  
XX PI Hartley JL, Brasch MA;  
XX  
XX DR WPI; 1997-065168/06.  
XX  
XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
PT using recombinant proteins and engineered recombination sites in vitro or  
PT in vivo.  
XX  
XX PS Claim 14; Page 55; 106pp; English.  
XX  
XX AAT48210-25 are att recombination site core region DNA sequences. The  
CC core region has at least one engineered mutation that enhances  
CC recombination in vitro in the formation of a Cointegrate or Product DNA.  
CC These core regions can be incorporated into novel vector donor DNA  
CC molecules. The nucleic acids, vectors and methods of the invention are  
CC used to obtain chimeric nucleic acid using recombination proteins and  
CC engineered recombination sites in vitro or in vivo. The improved  
CC specificity, speed and yields of the invention facilitates DNA or RNA  
CC subcloning, regulation or exchange useful for any related purpose, e.g.  
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
CC or modification of transcribed, replicated, isolated or genomic DNA or  
CC RNA  
XX  
XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;  
  
Query Match 80.0%; Score 20; DB 2; Length 25;  
Best Local Similarity 72.0%; Pred. No. 7.4;  
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 AGCCWGCCTTYKTRTACNAACTSGB 25  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 1 AGCCTGCTTTTGTGACAAACTTGT 25  
  
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Job time : 168.8 secs

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds  
(without alignments)  
494.978 Million cell updates/sec

Title: US-10-820-133-2

Perfect score: 25  
Sequence: 1 agcwgcttkttracnaactsgb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.2	84.8	25	3	US-09-233-493-2
2	21.2	84.8	25	3	US-09-005-476-2
3	21.2	84.8	25	3	US-09-233-492-2
4	21.2	84.8	25	3	US-09-296-280-2
5	21.2	84.8	25	4	US-09-498-074-2
6	21.2	84.8	25	4	US-09-498-074-2
7	21.2	84.8	25	5	PCT-US96-10082A-2
8	20.4	81.6	25	3	US-09-296-280-40
9	20	80.0	25	3	US-09-233-493-6
10	20	80.0	25	3	US-09-233-493-7
11	20	80.0	25	3	US-09-233-493-33
12	20	80.0	25	3	US-09-233-493-34
13	20	80.0	25	3	US-09-005-476-6
14	20	80.0	25	3	US-09-005-476-7
15	20	80.0	25	3	US-09-005-476-33
16	20	80.0	25	3	US-09-005-476-34
17	20	80.0	25	3	US-09-233-492-6
18	20	80.0	25	3	US-09-233-492-7
19	20	80.0	25	3	US-09-233-492-33
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22	20	80.0	25	3	US-09-296-280-7
23	20	80.0	25	4	US-09-498-074-6
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Sequence 33, Appli  
Sequence 34, Appli  
Sequence 6, Appli  
Sequence 7, Appli  
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Sequence 50, Appli  
Sequence 63, Appli  
Sequence 12, Appli  
Sequence 58, Appli  
Sequence 52, Appli  
Sequence 359, App  
Sequence 739, App  
Sequence 739, App  
Sequence 587, App  
Sequence 3, Appli

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32 20 80.0 25 5 PCT-US96-10082A-7  
c 33 20 80.0 48 3 US-09-296-280-56  
c 34 20 80.0 48 4 US-09-944-807-15  
c 35 20 80.0 49 3 US-09-296-280-50  
c 36 20 80.0 49 4 US-09-935-916B-63  
c 37 20 80.0 50 4 US-10-004-993A-12  
c 38 20 80.0 52 3 US-09-296-280-58  
c 39 20 80.0 53 3 US-09-296-280-52  
c 40 20 80.0 656 4 US-09-774-528-359  
c 41 20 80.0 970 4 US-09-636-215-739  
c 42 20 80.0 970 4 US-09-685-166A-739  
c 43 20 80.0 970 4 US-09-679-426-739  
c 44 20 80.0 1244 4 US-09-799-451-587  
c 45 20 80.0 1357 4 US-09-668-680-3

#### ALIGNMENTS

RESULT 1  
US-09-233-493-2  
; Sequence 2, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Braach, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
US-09-233-493-2



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Query Match      84.8%; Score 21.2; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
    |||||
Db 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 5
US-09-498-074-2
; Sequence 2, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-498-074-2

Query Match      84.8%; Score 21.2; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
    |||||
Db 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 6
US-09-498-074-2
; Sequence 2, Application US/09498074
; Patent No. 6720140
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-498-074-2

Query Match      84.8%; Score 21.2; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
    |||||
Db 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 7
PCT-US96-10082A-2
; Sequence 2, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-498-074-2
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```
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
RECOMBINATION SITES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: 04-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-498-074-2

Query Match      84.8%; Score 21.2; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
    |||||
Db 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 7
PCT-US96-10082A-2
; Sequence 2, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-498-074-2
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/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/10082A
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
PCT-US96-10082A-2

Query Match 84.8%; Score 21.2; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTTTCTACNAACTSGB 25
Db 1 AGCCGCTTTTCTACNAACTSGB 25

RESULT 8
US-09-296-280-40
/ Sequence 40, Application US/09296280
/ Patent No. 6277608
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ APPLICANT: Temple, Gary F.
/ APPLICANT: Fox, Donna K.
/ TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
/ TITLE OF INVENTION: Recombination Sites
/ FILE REFERENCE: 0942.285007
/ CURRENT APPLICATION NUMBER: US/09/296,280
/ EARLIER FILING DATE: 1999-04-22
/ EARLIER APPLICATION NUMBER: US 09/177,387
/ EARLIER FILING DATE: 1998-10-23
/ EARLIER APPLICATION NUMBER: US 60/065,930
/ EARLIER FILING DATE: 1997-10-24
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 40
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-296-280-40

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.37;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCCGCTTTTCTACNAACTSGB 25
Db 1 AGCCGCTTTTCTACNAACTSGB 25

RESULT 9
US-09-233-493-6
/ Sequence 6, Application US/09233493
/ Patent No. 6143557
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ TITLE OF INVENTION: Recombination Sites
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
```

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/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/233,493
/ FILING DATE: 20-JAN-1999
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
US-09-233-493-6

Query Match 80.0%; Score 20; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.59;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCGCTTTTCTACNAACTSGB 25
Db 1 AGCCGCTTTTCTACNAACTSGB 25

RESULT 10
US-09-233-493-7
/ Sequence 7, Application US/09233493
/ Patent No. 6143557
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ TITLE OF INVENTION: Recombination Sites
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/233,493  
FILING DATE: 20-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,476  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cdna  
US-09-233-493-7

Query Match 80.0%; Score 20; DB 3; Length 25;  
Best Local Similarity 72.0%; Pred. No. 0.59;  
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTKRTACNAACTSGB 25  
|||||:|||||:|||||:  
Db 1 AGCCTGCTTTCTGTACAACTGT 25

RESULT 11  
US-09-233-493-33/c  
Sequence 33, Application US/09233493  
Patent No. 6143557  
GENERAL INFORMATION:  
APPLICANT: Hartley, James L.  
APPLICANT: Brasch, Michael A.  
TITLE OF INVENTION: Recombinational Cloning Using Engineered  
TITLE OF INVENTION: Recombination Sites  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N. W. Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/233,493  
FILING DATE: 20-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,476  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995

CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cdna  
US-09-233-493-33

Query Match 80.0%; Score 20; DB 3; Length 25;  
Best Local Similarity 72.0%; Pred. No. 0.59;  
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTKRTACNAACTSGB 25  
|||||:|||||:|||||:  
Db 25 AGCCTGCTTTCTGTACAACTGT 1

RESULT 12  
US-09-233-493-34/c  
Sequence 34, Application US/09233493  
Patent No. 6143557  
GENERAL INFORMATION:  
APPLICANT: Hartley, James L.  
APPLICANT: Brasch, Michael A.  
TITLE OF INVENTION: Recombinational Cloning Using Engineered  
TITLE OF INVENTION: Recombination Sites  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N. W. Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/233,493  
FILING DATE: 20-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,476  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cdna  
US-09-233-493-34

Query Match 80.0%; Score 20; DB 3; Length 25;

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Best Local Similarity 72.0%; Pred. No. 0.59;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTKTRTACNAACTSGB 25
Db 25 AGCCGCTTTCTGTACAACTTGT 1

RESULT 13
US-09-005-476-6
; Sequence 6, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-7

Query Match 80.0%; Score 20; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.59;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTKTRTACNAACTSGB 25
Db 1 AGCCTGCTTTCTGTACAACTTGT 25

RESULT 15
US-09-005-476-33/c
; Sequence 33, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-6

Query Match 80.0%; Score 20; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.59;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTKTRTACNAACTSGB 25
Db 1 AGCCTGCTTTCTGTACAACTTGT 25

RESULT 14
US-09-005-476-7
; Sequence 7, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
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; MOLECULE TYPE: cDNA  
US-09-005-476-33

Query Match 80.0%; Score 20; DB 3; Length 25;  
Best Local Similarity 72.0%; Pred. No. 0.59;  
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTACNAACTSG 25  
|||:|||||:|||||:|||||:  
Db 25 AGCCTGCTTTTGTACAACTTGT 1

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Job time : 36.9 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 ; Search time 314 Seconds  
(without alignments)  
430.015 Million cell updates/sec

Title: US-10-820-133-2

Perfect score: 25

Sequence: 1 agcwgcttktactnaactsgb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	21.2	84.8	25	9	US-09-907-900-2
3	21.2	84.8	25	9	US-09-907-719-2
4	21.2	84.8	25	10	US-09-432-085-2
5	21.2	84.8	25	10	US-09-985-448-2
6	21.2	84.8	25	14	US-10-058-292-2
7	21.2	84.8	25	14	US-10-058-291-2
8	21.2	84.8	25	14	US-10-162-879-2
9	21.2	84.8	25	15	US-10-161-403-2
10	21.2	84.8	25	15	US-10-300-892-2
11	21.2	84.8	25	16	US-10-680-316-2
12	21.2	84.8	25	17	US-10-815-730-2

13	21.2	84.8	25	17	US-10-820-133-2	Sequence 2, Appli
14	21.2	84.8	25	18	US-10-161-408-34	Sequence 34, Appli
15	21.2	84.8	25	18	US-10-796-868A-2	Sequence 2, Appli
16	20.4	81.6	25	9	US-09-855-797A-40	Sequence 40, Appli
17	20.4	81.6	25	9	US-09-907-900-40	Sequence 40, Appli
18	20.4	81.6	25	9	US-09-907-719-40	Sequence 40, Appli
19	20.4	81.6	25	10	US-09-985-448-40	Sequence 40, Appli
20	20.4	81.6	25	15	US-10-300-892-40	Sequence 40, Appli
21	20.4	81.6	25	16	US-10-680-316-40	Sequence 40, Appli
22	20.4	81.6	25	17	US-10-815-730-40	Sequence 40, Appli
23	20.4	81.6	25	17	US-10-820-133-40	Sequence 40, Appli
24	20	80.0	25	9	US-09-732-914-5	Sequence 5, Appli
25	20	80.0	25	9	US-09-855-797A-6	Sequence 6, Appli
26	20	80.0	25	9	US-09-855-797A-7	Sequence 7, Appli
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28	20	80.0	25	9	US-09-907-900-7	Sequence 7, Appli
29	20	80.0	25	9	US-09-907-719-6	Sequence 6, Appli
30	20	80.0	25	9	US-09-907-719-7	Sequence 7, Appli
31	20	80.0	25	10	US-09-432-085-6	Sequence 6, Appli
32	20	80.0	25	10	US-09-432-085-7	Sequence 7, Appli
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38	20	80.0	25	14	US-10-055-001A-1	Sequence 1, Appli
39	20	80.0	25	14	US-10-055-001A-2	Sequence 2, Appli
40	20	80.0	25	14	US-10-058-292-6	Sequence 6, Appli
41	20	80.0	25	14	US-10-058-292-7	Sequence 7, Appli
42	20	80.0	25	14	US-10-058-292-33	Sequence 33, Appli
43	20	80.0	25	14	US-10-058-292-34	Sequence 34, Appli
44	20	80.0	25	14	US-10-058-291-6	Sequence 6, Appli
45	20	80.0	25	14	US-10-058-291-7	Sequence 7, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-855-797A-2  
; Sequence 2, Application US/09855797A  
; Patent No. US20020094574A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.285008  
; CURRENT APPLICATION NUMBER: US/09/855.797A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/296,281  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-855-797A-2

Query Match 84.8%; Score 21.2; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



RESULT 5  
US-09-985-448-2  
; Sequence 2, Application US/09985448  
; Publication No. US20030157716A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/985,448  
; CURRENT FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-985-448-2

Query Match 84.8%; Score 21.2; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTKRTACNACTSGB 25  
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Db 1 AGCCGCTTTTKRTACNACTSGB 25

RESULT 6  
US-10-058-292-2  
; Sequence 2, Application US/10058292  
; Publication No. US2003005452A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; RECOMBINATION SITES  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/058,292  
; FILING DATE: 30-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/432,085  
; FILING DATE: 1999-11-02  
; APPLICATION NUMBER: 09/233,493  
; FILING DATE: 1999-11-02  
; APPLICATION NUMBER: 09/233,493  
; FILING DATE: 20-JAN-1999

; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-058-292-2

Query Match 84.8%; Score 21.2; DB 14; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCCGCTTTTKRTACNACTSGB 25

RESULT 7  
US-10-058-291-2  
; Sequence 2, Application US/10058291  
; Publication No. US20030064515A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; RECOMBINATION SITES  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/058,291  
; FILING DATE: 30-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/432,085  
; FILING DATE: 1999-11-02  
; APPLICATION NUMBER: 09/233,493  
; FILING DATE: 20-JAN-1999  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both

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; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-058-291-2

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Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCCWGCCTTYYKTRTACNAACTSG 25

RESULT 8
US-10-162-879-2
; Sequence 2, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-162-879-2

Query Match      84.8%; Score 21.2; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCCWGCCTTYYKTRTACNAACTSG 25
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RESULT 9
US-10-161-403-42
; Sequence 42, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Steward, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: m-attB;
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: 18
; OTHER INFORMATION: n is a o r g o r t/u
US-10-161-403-42

Query Match      84.8%; Score 21.2; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSG 25
Db 1 AGCCWGCCTTYYKTRTACNAACTSG 25

RESULT 10
US-10-300-892-2
; Sequence 2, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
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RESULT 12
US-10-815-730-2
; Sequence 2, Application US/10815730
; Publication NO. US20040171156A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary P.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/815,730
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24

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: RESULT 14
US-10-161-408-34
; Sequence 34, Application US/10161408
; Publication No. US20040214290A1
; GENERAL INFORMATION:
; APPLICANT: Perez, Carl
; APPLICANT: Fabijanski, Steven

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Job time : 315.1 secs

APPLICANT: Perkins, Edward  
TITLE OF INVENTION: Plant Artificial Chromosomes, Uses thereof, and Methods of Preparation  
FILE REFERENCE: 24601-419  
CURRENT APPLICATION NUMBER: US/10/161,408  
CURRENT FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: US 60/294,687  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: US 60/296,329  
PRIOR FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 34  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: m-attB recognition sequence  
NAME/KEY: misc\_difference  
LOCATION: 18  
OTHER INFORMATION: n is a or c or g or t/u  
US-10-161-408-34

Query Match 84.8%; Score 21.2; DB 18; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSG 25  
Db 1 AGCCWGCCTTYYKTRTACNAACTSG 25

## RESULT 15

US-10-796-868A-2  
Sequence 2, Application US/10796868A  
Publication No. US20040219673A1  
GENERAL INFORMATION:  
APPLICANT: Braesch, Michael A.  
TITLE OF INVENTION: Recombinational Cloning Using Engineered Recombination Sites  
FILE REFERENCE: 0942.285000K  
CURRENT APPLICATION NUMBER: US/10/796,868A  
CURRENT FILING DATE: 2004-03-10  
PRIOR APPLICATION NUMBER: US 09/498,074  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 09/005,476  
PRIOR FILING DATE: 1998-01-12  
PRIOR APPLICATION NUMBER: US 08/663,002  
PRIOR FILING DATE: 1996-06-07  
PRIOR APPLICATION NUMBER: US 08/486,139  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: m-attB core region  
NAME/KEY: misc\_feature  
LOCATION: (18)-(18)  
OTHER INFORMATION: n is a, c, g, or t/u  
US-10-796-868A-2

Query Match 84.8%; Score 21.2; DB 18; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSG 25  
Db 1 AGCCWGCCTTYYKTRTACNAACTSG 25

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds  
(without alignments)  
594.643 Million cell updates/sec

Title: US-10-820-133-2

Perfect score: 25

Sequence: 1 agccwgcttcttactaactagb 25

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hcc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.2	84.8	888	7	CK209237
2	21.2	84.8	1012	7	CK211630
3	21.2	84.8	1031	7	CK163965
4	21.2	84.8	1031	7	CK212789
5	21.2	84.8	1043	7	CK212830
6	21.2	84.8	1051	7	CK212815
7	21.2	84.8	1053	7	CK212320
8	21.2	84.8	1059	7	CK163940
9	21.2	84.8	1062	7	CK212429
10	21.2	84.8	1067	7	CK212431
11	21.2	84.8	1070	7	CK213073
12	21.2	84.8	1071	7	CK211886
13	21.2	84.8	1071	7	CK212465
14	21.2	84.8	1076	7	CK216054
15	21.2	84.8	1082	7	CK212170
16	21.2	84.8	1088	7	CK205724
17	21.2	84.8	1093	7	CK211774
18	21.2	84.8	1095	7	CK212335
19	21.2	84.8	1098	7	CK213245
20	21.2	84.8	1102	7	CK214856
21	21.2	84.8	1113	7	CK207537
22	21.2	84.8	1113	7	CK216493
23	21.2	84.8	1119	7	CK214588
24	21.2	84.8	1124	7	CK211806

25	21.2	84.8	1147	7	CK211595
26	21.2	84.8	1156	7	CK205566
27	21.2	84.8	1175	7	CK211649
28	20	80.0	83	6	CB398074
29	20	80.0	83	6	CB401650
30	20	80.0	109	6	CB103959
31	20	80.0	141	6	CB103917
32	20	80.0	190	4	BI477091
33	20	80.0	201	4	BG775739
34	20	80.0	214	5	EX347917
35	20	80.0	221	6	CB104038
36	20	80.0	223	5	EX347916
37	20	80.0	275	7	CK447077
38	20	80.0	281	2	BE612945
39	20	80.0	307	7	CF857529
40	20	80.0	336	5	BP776084
41	20	80.0	337	2	BE672796
42	20	80.0	347	4	BI446328
43	20	80.0	358	6	CB103951
44	20	80.0	363	6	CB103941
45	20	80.0	367	5	BP776789

## ALIGNMENTS

RESULT 1  
CK209237  
LOCUS  
DEFINITION FGAS020994 Triticum aestivum FGAS: Library 5 GATE 7 Triticum  
aestivum CDNA, mRNA sequence.  
CK209237  
CK209237.1 GI:39571627  
EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum

REFERENCE  
AUTHORS  
Allard, F., Crosby, W.L., Danyluk, J., Eudes, P., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D., Penniket, C., Roach, J.L., and Sarhan, F.  
Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
Unpublished (2003)  
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1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033  
Email: fgas\_esta@cs.usask.ca

FEATURES  
source  
1. .888  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone\_lib="Triticum aestivum FGAS: Library 5 GATE 7"  
/note="Vector: pCMV.SPORT6; Crown and developmental stages of spike formation in wheat cultivar Norstar. 4 mRNA populations were combined before constructing the library. The first mRNA population is from 1cm crown sections after 30 days of cold acclimation. The second is from 1cm crown sections after 11 days of deacclimation (before deacclimation plants were fully vernalized for 49 days)."

CK211595 FGAS02344  
CK205566 FGAS01707  
CK211649 FGAS02350  
CB398074 OSTF197D3  
CB401650 OSTF197D3  
CB103959 ADP\_SQ013  
CB103917 ADP\_SQ013  
BI477091 dal29h07.  
BG775739 602650134  
BX347917 BX347917  
CB104038 ADP\_SQ015  
BX347916 BX347916  
BI446328 dal87a02.  
BE612945 601451890  
BE612945 601451890  
CF857529 p8MLU005XK  
BP776084 BP776084  
BE672796 7b77g06.x  
BI446328 dal87a02.  
CB103951 ADP\_SQ013  
CB103941 ADP\_SQ013  
BP776789 BP776789

CK209237 888 bp mRNA linear EST 08-DEC-2003  
FGAS020994 Triticum aestivum FGAS: Library 5 GATE 7 Triticum  
aestivum CDNA, mRNA sequence.  
CK209237  
CK209237.1 GI:39571627  
EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.  
1 (bases 1 to 888)  
Allard, F., Crosby, W.L., Danyluk, J., Eudes, P., Frick, M., Gaudet, D.,  
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,  
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,  
Penniket, C., Roach, J.L., and Sarhan, F.  
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Unpublished (2003)  
Contact: Wm L Crosby  
Bioinformatics  
University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033  
Email: fgas\_esta@cs.usask.ca  
This sequence is the direct result of the Base calling software  
Phred (default parameters). It is the raw base calls. To aid in the  
identification of the high quality insert the software Lucy  
(default parameters) has been run on this sequence. Lucy identified  
the region [11,663].  
Plate: L5B016 row: N column: 13.  
Location/Qualifiers  
1. .888  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone\_lib="Triticum aestivum FGAS: Library 5 GATE 7"  
/note="Vector: pCMV.SPORT6; Crown and developmental stages  
of spike formation in wheat cultivar Norstar. 4 mRNA  
populations were combined before constructing the library.  
The first mRNA population is from 1cm crown sections after  
30 days of cold acclimation. The second is from 1cm crown  
sections after 11 days of deacclimation (before  
deacclimation plants were fully vernalized for 49 days)."



later, consisted of live crown and leaf tissue (leaf tissue that was yellow was not included in sampled material). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."

ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1031;  
Best Local Similarity 72.0%; Pred. No. 24;  
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 1 AGCCGCTTTTCTACNAACTSG 25

Db 738 AGCTGCTTTTGTACAACTGGT 762

RESULT 4

CK212789

LOCUS CK212789 1031 bp mRNA linear EST 09-DEC-2003  
DEFINITION FGAS024677 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum  
aestivum cDNA, mRNA sequence.

ACCESSION

CK212789

CK212789.1 GI:39618893

KEYWORDS

EST.

SOURCE

ORGANISM

Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

1 (bases 1 to 1031)

Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,

Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,

Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,

Penniket, C., Roach, J.L. and Sarhan, F.

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Unpublished (2003)

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Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769

Fax: 306 966 2033

Email: fgas\_est@cs.usask.ca

This sequence is the direct result of the Base calling software

Phred (default parameters). It is the raw base calls. To aid in the

identification of the high quality insert the software Lucy

(default parameters) has been run on this sequence. Lucy identified

the region [69,774].

Plate: L6B006 row: P column: 06.

Location/Qualifiers

1..1031

/organism="Triticum aestivum"

/mol\_type="mRNA"

/db\_xref="taxon:4565"

/clone\_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"

/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown

(50%) and leaf (50%) tissues from wheat cultivar Norstar

after short exposure times to low temperature in the light

and in the dark. 12 mRNA populations were combined before

constructing the library. The first 6 populations: After 7

days of growth at 20°C from wheat cultivar Norstar after

short exposure times to low temperature in the light and

in the dark. 12 mRNA populations were combined before

constructing the library. The first 6 populations: After 7

days of growth at 20, wheat plants were transferred to 4C

in the light. 1cm crown sections and green leaf tissue were

separately harvested after 1, 3, and 6 hours of low

temperature exposure. First strand synthesis in this

library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACTGAGCAGGAGGACACTGACATGAGGAGTAGAAA)."

ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1031;

Best Local Similarity 72.0%; Pred. No. 24;

Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 1 AGCCGCTTTTCTACNAACTSG 25

Db 809 AGCTGCTTTTGTACAACTGGT 833

RESULT 5

CK212830

LOCUS CK212830 1043 bp mRNA linear EST 09-DEC-2003  
DEFINITION FGAS024720 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum  
aestivum cDNA, mRNA sequence.

ACCESSION

CK212830

CK212830.1 GI:39618934

KEYWORDS

EST.

SOURCE

ORGANISM

Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

1 (bases 1 to 1043)

Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,

Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,

Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,

Penniket, C., Roach, J.L. and Sarhan, F.

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Unpublished (2003)

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Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769

Fax: 306 966 2033

Email: fgas\_est@cs.usask.ca

This sequence is the direct result of the Base calling software

Phred (default parameters). It is the raw base calls. To aid in the

identification of the high quality insert the software Lucy

(default parameters) has been run on this sequence. Lucy identified

the region [24,647].

Plate: L6B007 row: C column: 18.

Location/Qualifiers

1..1043

/organism="Triticum aestivum"

/mol\_type="mRNA"

/db\_xref="taxon:4565"

/clone\_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"

/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown

(50%) and leaf (50%) tissues from wheat cultivar Norstar

after short exposure times to low temperature in the light

and in the dark. 12 mRNA populations were combined before

constructing the library. The first 6 populations: After 7

days of growth at 20°C from wheat cultivar Norstar after

short exposure times to low temperature in the light and

in the dark. 12 mRNA populations were combined before

constructing the library. The first 6 populations: After 7

days of growth at 20, wheat plants were transferred to 4C

in the light. 1cm crown sections and green leaf tissue were

separately harvested after 1, 3, and 6 hours of low



after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20°Cs from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4°C in the light. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20°C, wheat plants were transferred to 4°C in the dark. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACTGGACGACGACATGACATGACTGAGGATGAGAA)."

## ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1053;  
Best Local Similarity 72.0%; Pred. No. 24;  
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTTACNAACTSG 25  
||||:||||:||||:||||:||||:  
Db 819 AGCCTGCTTTTGTACAACTGCT 843

## RESULT 8

CK163940  
LOCUS  
DEFINITION CK163940 1059 bp mRNA linear EST 05-DEC-2003  
aestivum cDNA, mRNA sequence.

ACCESSION CK163940  
VERSION  
KEYWORDS  
SOURCE

ORGANISM  
Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.

1 (bases 1 to 1059)

REFERENCE  
AUTHORS Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D., Penniket, C., Roach, J.L. and Sarhan, A.

Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
Unpublished (2003)

CONTACT: Wm L Crosby

INSTITUTION: Bioinformatics

UNIVERSITY: University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada

TEL: 306 966 1769

FAX: 306 966 2033

EMAIL: fgas\_est@cs.usask.ca

This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [85,522].

Plate: L4B009, row: L column: 17.

Location/Qualifiers

1..1059

/organism="Triticum aestivum"

## FEATURES

source

/mol\_type="mRNA"

/db\_xref="taxon:4565"

/clone\_lib="Triticum aestivum FGAS: Library 4 Gate 8"

/note="Organ: Crown and leaf; Vector: pCMV.SPORT6;

Conditions for growth: Seeds were germinated in a water-saturated mix (50% black earth and 50% ProMix) in a growth chamber for 7 days under an irradiance of 200 mmol m<sup>-2</sup> sec<sup>-1</sup>. The temperature was maintained at 20 degrees C with a 15-hr photoperiod under a relative humidity of 70%. After this period watering of plants was stopped. Four time points were sampled during a two week period; the first after wilting was observed and the last, two weeks later, consisted of live crown and leaf tissue (leaf tissue that was yellow was not included in sampled material). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."

## ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1059;  
Best Local Similarity 72.0%; Pred. No. 24;  
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTTACNAACTSG 25  
||||:||||:||||:||||:||||:  
Db 557 AGCCTGCTTTTGTACAACTGCT 581

## RESULT 9

CK212429  
LOCUS  
DEFINITION CK212429 1062 bp mRNA linear EST 09-DEC-2003  
aestivum cDNA, mRNA sequence.

ACCESSION CK212429  
VERSION  
KEYWORDS  
SOURCE

ORGANISM  
Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.

1 (bases 1 to 1062)

REFERENCE  
AUTHORS Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D., Penniket, C., Roach, J.L. and Sarhan, A.

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Unpublished (2003)

CONTACT: Wm L Crosby

INSTITUTION: Bioinformatics

UNIVERSITY: University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada

TEL: 306 966 1769

FAX: 306 966 2033

EMAIL: fgas\_est@cs.usask.ca

This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [42,723].

Plate: L6B005, row: K column: 03.

Location/Qualifiers

1..1062

/organism="Triticum aestivum"

/mol\_type="mRNA"

/db\_xref="taxon:4565"

/clone\_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"  
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown (50%) and leaf (50%) tissues from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7

days of growth at 20°Cs from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4°C in the light. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20°C, wheat plants were transferred to 4°C in the dark. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACTGGAGCAGGACACACGACATGCGACTGAGGAGTAGAAA)."

## ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1062;  
 Best Local Similarity 72.0%; Pred. No. 24;  
 Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSG 25

Db 791 AGCCTGCTTTTGTACAACTGGT 815

## RESULT 10

CK212431 1067 bp mRNA linear EST 09-DEC-2003  
 LOCUS FGAS024303 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum  
 DEFINITION aestivum cDNA, mRNA sequence.

ACCESSION CK212431

VERSION CK212431.1 GI:39618535

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.

1 (bases 1 to 1067)

ALLARD, F., CROSBY, W. L., DANYLUK, J., Eudes, F., Frick, M., Gaudet, D.,  
 Genswein, B., Graf, R., Gulick, P., Hrycan, L. D., Laroche, A.,  
 Links, M. G., McCarthy, E. L., Monroy, A., Muzak, I., Nilsson, D.,  
 Penniket, C., Roach, J. L. and Sarhan, F.

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 Unpublished (2003)

Contact: Wm L Crosby

Bioinformatics

University of Saskatchewan, Department of Computer Science

1C101 Engineering Building, 57 Campus Drive, Saskatoon,

Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769

Fax: 306 966 2033

Email: fgas\_estsecs.usask.ca

This sequence is the direct result of the Base calling software  
 Phred (default parameters). It is the raw base calls. To aid in the  
 identification of the high quality insert the software Lucy  
 (default parameters) has been run on this sequence. Lucy identified  
 the region [22,802].

Plate: L6B005 row: K column: 05.

Location/Qualifiers

1..1067

/organism="Triticum aestivum"

/mol\_type="mRNA"

/db\_xref="caxon:4565"

/clone\_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"

## FEATURES

source

/note="Organ: Crown and leaf; Vector: pCMV.SP0RT6; Crown (50%) and leaf (50%) tissues from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20°Cs from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4°C in the light. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20°C, wheat plants were transferred to 4°C in the dark. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACTGGAGCAGGACACACGACATGCGACTGAGGAGTAGAAA)."

## ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1067;  
 Best Local Similarity 72.0%; Pred. No. 24;  
 Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSG 25

Db 871 AGCCTGCTTTTGTACAACTGGT 895

## RESULT 11

CK213073 1070 bp mRNA linear EST 09-DEC-2003  
 LOCUS FGAS024975 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum  
 DEFINITION aestivum cDNA, mRNA sequence.

ACCESSION CK213073

VERSION CK213073.1 GI:39619177

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.

1 (bases 1 to 1070)

ALLARD, F., CROSBY, W. L., DANYLUK, J., Eudes, F., Frick, M., Gaudet, D.,  
 Genswein, B., Graf, R., Gulick, P., Hrycan, L. D., Laroche, A.,  
 Links, M. G., McCarthy, E. L., Monroy, A., Muzak, I., Nilsson, D.,  
 Penniket, C., Roach, J. L. and Sarhan, F.

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Unpublished (2003)

Contact: Wm L Crosby

Bioinformatics

University of Saskatchewan, Department of Computer Science

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Fax: 306 966 2033

Email: fgas\_estsecs.usask.ca

This sequence is the direct result of the Base calling software  
 Phred (default parameters). It is the raw base calls. To aid in the  
 identification of the high quality insert the software Lucy  
 (default parameters) has been run on this sequence. Lucy identified  
 the region [22,640].

Plate: L6B008 row: B column: 07.

Location/Qualifiers

## FEATURES



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source
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/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
(note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown
(50%) and leaf (50%) tissues from wheat cultivar Norstar
after short exposure times to low temperature in the light
and in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20°C from wheat cultivar Norstar after
short exposure times to low temperature in the light and
in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20, wheat plants were transferred to 4°C
in the light. 1cm crown sections and green leaf tissue were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. The last 6 populations: After 7 days
of growth at 20°C, wheat plants were transferred to 4°C in
the dark. 1cm crown sections and green leaf tissue were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. First strand synthesis in this
library was done in the presence of methylated dCTP
thereby protecting from internal cleavage with NotI. In
addition, this library used a primer for second strand
synthesis that annealed to an artificial sequence (RNA
oligo) added before first strand synthesis. Therefore when
sequences from EST generated from this library will be
masked for vector and adaptor sequences, an additional
masking step will have to be included to mask this RNA
oligo that is common to all clones (sequence
CGACTGGAGCAGGAGACATGACATGAGGAGTAGAAA)."

ORIGIN
Query Match      84.8%; Score 21.2; DB 7; Length 1070;
Best Local Similarity 72.0%; Pred. No. 24;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTCNAACTG 25
|||||:|||||:|||||:|||||:
Db 675 AGCCTGCTTTTGTACAACTG 699

RESULT 12
CK211886
LOCUS
DEFINITION
CK211886 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum
aestivum cDNA, mRNA sequence.
ACCESSION
CK211886.1 GI:39617990
VERSION
CK211886.1
KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 1071)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Larocque, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science,
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_est@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the

identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [12,834].
Plate: L6B003 row: L column: 24.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
(note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown
(50%) and leaf (50%) tissues from wheat cultivar Norstar
after short exposure times to low temperature in the light
and in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20°C from wheat cultivar Norstar after
short exposure times to low temperature in the light and
in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20, wheat plants were transferred to 4°C
in the light. 1cm crown sections and green leaf tissue were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. The last 6 populations: After 7 days
of growth at 20°C, wheat plants were transferred to 4°C in
the dark. 1cm crown sections and green leaf tissue were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. First strand synthesis in this
library was done in the presence of methylated dCTP
thereby protecting from internal cleavage with NotI. In
addition, this library used a primer for second strand
synthesis that annealed to an artificial sequence (RNA
oligo) added before first strand synthesis. Therefore when
sequences from EST generated from this library will be
masked for vector and adaptor sequences, an additional
masking step will have to be included to mask this RNA
oligo that is common to all clones (sequence
CGACTGGAGCAGGAGACATGACATGAGGAGTAGAAA)."

ORIGIN
Query Match      84.8%; Score 21.2; DB 7; Length 1071;
Best Local Similarity 72.0%; Pred. No. 24;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTCNAACTG 25
|||||:|||||:|||||:|||||:
Db 925 AGCCTGCTTTTGTACAACTG 949

RESULT 13
CK212465
LOCUS
DEFINITION
CK212465 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum
aestivum cDNA, mRNA sequence.
ACCESSION
CK212465
VERSION
CK212465.1 GI:39618569
KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 1071)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Larocque, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
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Email: fgas_est@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the

```

Contact: Wm L Crosby  
Bioinformatics  
University of Saskatchewan, Department of Computer Science  
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Email: fgas\_esta@cs.usask.ca

```

phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [16,760].
Plate: L6B020 row: L column: 02.

FEATURES             Location/Qualifiers
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     /db_xref="taxon:4565"
     /clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
     /note="Organ: Crown and leaf; Vectors: pCMV.SPORTS; Crown
     (50%) and leaf (50%) tissues from wheat cultivar Norstar
     after short exposure times to low temperature in the light
     and in the dark. 12 mRNA populations were combined before
     constructing the library. The first 6 populations: After 7
     days of growth at 20Cs from wheat cultivar Norstar after
     short exposure times to low temperature in the light and
     in the dark. 12 mRNA populations were combined before
     constructing the library. The first 6 populations: After 7
     days of growth at 20, wheat plants were transferred to 4C
     in the light. 1cm crown sections and green leaf tissue were
     separately harvested after 1, 3, and 6 hours of low
     temperature exposure. The last 6 populations: After 7 days
     of growth at 20C, wheat plants were transferred to 4C in
     the dark. 1cm crown sections and green leaf tissue were
     separately harvested after 1, 3, and 6 hours of low
     temperature exposure. First strand synthesis in this
     library was done in the presence of methylated dCTP
     thereby protecting from internal cleavage with NotI. In
     addition, this library used a primer for second strand
     synthesis that annealed to an artificial sequence (RNA
     oligo) added before first strand synthesis. Therefore when

```

ORIGIN	Query Match	Best Local Similarity	Score	DB	Length
<p>sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACTGGACACGAGCACTGACATGGCTGAAGGATGAAA)." 84.8%;</p>	72.0%;	21.2;	7;	1076;	

Qy 1 AGCGWGCCTTYYKTRTACNAACTSGB 25  
 ||||:||||:||||:||||:|  
 Db 822 AGCGTCTTTTTTGTACAAACTGGT 846

RESULT 15  
 CK212170  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

CK212170 1082 bp mRNA linear EST 09-DEC-2003  
 FGAS024038 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum  
 aestivum cDNA, mRNA sequence.  
 CK212170  
 CK212170.1 GI:39618274  
 EST.  
 Triticum aestivum (bread wheat)  
 Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooidae; Triticeae; Triticum.  
 1 (bases 1 to 1082)  
 Allard, R., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,

REFERENCE  
 AUTHORS

Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,  
 Links, M.G., McCarthy, E.B., Monroy, A., Muzak, I., Nilsson, D.,  
 Penniket, C., Roach, J.L. and Sarhan, F.  
 Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
 Unpublished (2003)  
 Contact: Wm L Crosby  
 Bioinformatics  
 University of Saskatchewan, Department of Computer Science  
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
 Saskatchewan, S7N 5A9, Canada  
 Tel: 306 966 1769  
 Fax: 306 966 2033  
 Email: fgas\_est@cs.usask.ca

TITLE  
 JOURNAL  
 COMMENT

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 Phred (default parameters). It is the raw base calls. To aid in the  
 identification of the high quality insert the software Lucy  
 (default parameters) has been run on this sequence. Lucy identified  
 the region [39,712].  
 Plate: LEB004 row: L column: 06.

FEATURES  
 source

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    /mol_type="mRNA"
    /db_xref="taxon:4565"
    /clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
    /note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown
(50%) and leaf (50%) tissues from wheat cultivar Norstar
after short exposure times to low temperature in the light
and in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20C from wheat cultivar Norstar after
short exposure times to low temperature in the light and
in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20, wheat plants were transferred to 4C
in the light. 1cm crown sections and green leaf tissue were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. The last 6 populations: After 7 days
of growth at 20C, wheat plants were transferred to 4C in
the dark. 1cm crown sections and green leaf tissue were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. First strand synthesis in this
library was done in the presence of methylated dCTP
thereby protecting from internal cleavage with NotI. In
addition, this library used a primer for second strand
synthesis that annealed to an artificial sequence (RNA
oligo) added before first strand synthesis. Therefore when
sequences from EST generated from this library will be
masked for vector and adaptor sequences, an additional
masking step will have to be included to mask this RNA
oligo that is common to all clones (sequence
CGACTGGAGCAGGAGACACTGCATGCATGAGGAGTAGAAA)."
```

ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1082;  
 Best Local Similarity 72.0%; Pred. NO. 24;  
 Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTTACNACTSGB 25

Db 815 AGCCTGCTTTTGTGTACNACTGTT 839

Search completed: November 16, 2004, 10:16:29  
 Job time : 1534 secs

This Page Blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:43 ; Search time 708.5 Seconds  
(without alignments)  
1668.656 Million cell updates/sec

Title: US-10-820-133-3

Perfect score: 25  
Sequence: 1 gttcagctttctkrtacnaactsgb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	88.0	25	6	AR124523 Sequence
2	22	88.0	25	6	AR163174 Sequence
3	22	88.0	25	6	AR493775 Sequence
4	22	88.0	25	6	AX269133 Sequence
5	22	88.0	25	6	AX491642 Sequence
6	22	88.0	25	6	AX498613 Sequence
7	22	88.0	25	6	BD131329 Recombina
8	21.2	84.8	25	6	BD131368 Recombina
9	20.8	83.2	25	6	AR124530 Sequence
10	20.8	83.2	25	6	AR163181 Sequence
11	20.8	83.2	25	6	AR493782 Sequence
12	20.8	83.2	25	6	AX491649 Sequence
13	20.8	83.2	25	6	AX498620 Sequence
14	20.8	83.2	25	6	BD131336 Recombina
15	20.8	83.2	43	6	BD263260 Compositi
16	20.4	81.6	25	6	AX787513 Sequence
17	20.4	81.6	25	6	BD131337 Recombina
18	20.4	81.6	37	6	CQ758822 Sequence
19	20.4	81.6	102	6	BD263460 Compositi

20	20.4	81.6	102	6	BD263462	Compositi
21	20.4	81.6	135	6	BD263228	Compositi
22	20.4	81.6	153	6	BD263458	Compositi
23	20.4	81.6	204	6	BD263433	Compositi
24	20.4	81.6	255	6	BD263435	Compositi
25	20.4	81.6	1846	6	AX703501	Sequence
26	20.4	81.6	4252	12	AY423865	Cloning v
27	20.4	81.6	4462	12	VF055134	Transfect
28	20.4	81.6	4554	6	BD263394	Compositi
29	20.4	81.6	5148	6	AX306327	Sequence
30	20.4	81.6	5558	6	CQ794769	Sequence
31	20.4	81.6	5848	6	BD263361	Compositi
32	20.4	81.6	5957	6	BD263353	Compositi
33	20.4	81.6	5957	6	BD263354	Compositi
34	20.4	81.6	6025	6	BD263355	Compositi
35	20.4	81.6	6264	6	BD263371	Compositi
36	20.4	81.6	6354	6	BD263365	Compositi
37	20.4	81.6	6422	6	BD263362	Compositi
38	20.4	81.6	6464	6	BD263349	Compositi
39	20.4	81.6	6526	6	BD263356	Compositi
40	20.4	81.6	6553	6	BD263350	Compositi
41	20.4	81.6	6613	6	BD263366	Compositi
42	20.4	81.6	6652	6	BD263373	Compositi
43	20.4	81.6	6668	6	BD263367	Compositi
44	20.4	81.6	6675	6	BD263364	Compositi
45	20.4	81.6	6708	6	BD263358	Compositi

ALIGNMENTS

RESULT 1	AR124523	Sequence 3 from patent US 6171861.	25 bp	DNA	linear	PAT 16-MAY-2001
LOCUS	AR124523					
DEFINITION	Sequence 3 from patent US 6171861.					
ACCESSION	AR124523					
VERSION	AR124523.1	GI:14109884				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 25)					
AUTHORS	Hartley, J.L. and Brasch, M.A.					
TITLE	Recombinational cloning using engineered recombination sites					
JOURNAL	Patent: US 6171861-A 3 09-JAN-2001;					
FEATURES	Location/Qualifiers					
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LOCUS	AR163174					
DEFINITION	Sequence 3 from patent US 6270969.					
ACCESSION	AR163174					
VERSION	AR163174.1	GI:16233681				
KEYWORDS	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 25)					
AUTHORS	Hartley, J.L. and Brasch, M.A.					
TITLE	Recombinational cloning using engineered recombination sites					

JOURNAL Patent: US 6270969-A 3 07-AUG-2001;  
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ORIGIN

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DB 1 GTTCAGCTTCTCKTRTACNAACTSGB 25

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AX493775  
LOCUS AR493775 25 bp mRNA linear PAT 15-MAY-2004  
DEFINITION Sequence 3 from patent US 6720140.  
ACCESSION AR493775  
VERSION AR493775.1 GI:472666186  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley, J.L. and Brasch, M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: US 6720140-A 3 13-APR-2004;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="mRNA"

ORIGIN

Query Match 88.0%; Score 22; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCKTRTACNAACTSGB 25  
|||||  
DB 1 GTTCAGCTTCTCKTRTACNAACTSGB 25

RESULT 4  
AX269133  
LOCUS AX269133 25 bp DNA linear PAT 29-OCT-2001  
DEFINITION Sequence 4 from Patent WO0174861.  
ACCESSION AX269133  
VERSION AX269133.1 GI:16542053  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Ville, R.G., Harrington, K., Murphy, S. and Bateman, A.  
TITLE Compositions and methods for tissue specific gene regulation  
JOURNAL therapy  
Patent: WO 0174861-A 4 11-OCT-2001;  
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)  
FEATURES Location/Qualifiers  
source 1..25  
/organism="synthetic construct"  
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/note="Synthetically generated vector sequence"

ORIGIN

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

JOURNAL Patent: US 6270969-A 3 07-AUG-2001;  
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ORIGIN

Query Match 88.0%; Score 22; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCKTRTACNAACTSGB 25  
|||||  
DB 1 GTTCAGCTTCTCKTRTACNAACTSGB 25

RESULT 5  
AX491642  
LOCUS AX491642 25 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 3 from Patent EP1227147.  
ACCESSION AX491642  
VERSION AX491642.1 GI:22324150  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1  
AUTHORS Hartley, J.L. and Brasch, M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: EP 1227147-A 3 31-JUL-2002;  
INVITROGEN CORPORATION (US)  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 88.0%; Score 22; DB 6; Length 25;  
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCKTRTACNAACTSGB 25  
|||||  
DB 1 GTTCAGCTTCTCKTRTACNAACTSGB 25

RESULT 6  
AX498613  
LOCUS AX498613 25 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 3 from Patent EP1229113.  
ACCESSION AX498613  
VERSION AX498613.1 GI:23343410  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1  
AUTHORS Hartley, J.L. and Brasch, M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: EP 1229113-A 3 07-AUG-2002;  
INVITROGEN CORPORATION (US)  
FEATURES Location/Qualifiers  
source 1..25  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 88.0%; Score 22; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCKTRTACNAACTSGB 25  
|||||  
DB 1 GTTCAGCTTCTCKTRTACNAACTSGB 25

RESULT 7  
BD131329  
LOCUS BD131329 25 bp DNA linear PAT 18-SEP-2002  
DEFINITION Recombinational cloning using nucleic acids having recombination sites.  
ACCESSION BD131329



ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: US 6720140-A 10 13-APR-2004;  
FEATURES Location/Qualifiers  
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ORIGIN

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Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25  
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Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 12  
LOCUS AX491649 25 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 10 from Patent EP1227147.  
ACCESSION AX491649  
VERSION AX491649.1 GI:22324157  
KEYWORDS .  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: EP 1227147-A 10 31-JUL-2002;  
JOURNAL INVITROGEN CORPORATION (US)

FEATURES Location/Qualifiers  
source 1..25  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 83.2%; Score 20.8; DB 6; Length 25;  
Best Local Similarity 80.0%; Pred. No. 8.3;  
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25  
|||||:|||||:|||||:  
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 13  
LOCUS AX498620 25 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 10 from Patent EP1229113.  
ACCESSION AX498620  
VERSION AX498620.1 GI:233343417  
KEYWORDS .  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: EP 1229113-A 10 07-AUG-2002;  
JOURNAL INVITROGEN CORPORATION (US)

FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 83.2%; Score 20.8; DB 6; Length 25;  
Best Local Similarity 80.0%; Pred. No. 8.3;  
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25  
|||||:|||||:|||||:  
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 14  
LOCUS BD131336 25 bp DNA linear PAT 18-SEP-2002  
DEFINITION Recombinational cloning using nucleic acids having recombination sites.  
ACCESSION BD131336  
VERSION BD131336.1 GI:23226281  
KEYWORDS JP 2002500861-A/10.  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.  
TITLE Recombinational cloning using nucleic acids having recombination sites.  
JOURNAL Patent: JP 2002500861-A 10 15-JAN-2002;  
JOURNAL LIFE TECHNOLOGIES INC  
COMMENT OS Unknown  
PN JP 2002500861-A/10  
PD 15-JAN-2002  
PF 26-OCT-1998 JP 2000518069  
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI  
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC  
C12N15/09, C12O1/68, C12N15/00  
CC Description of Unknown Organism: recombination products FH  
Key source Location/Qualifiers  
FT 1..25  
/organism='Unknown'.  
FEATURES Location/Qualifiers  
source 1..25  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 83.2%; Score 20.8; DB 6; Length 25;  
Best Local Similarity 80.0%; Pred. No. 8.3;  
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25  
|||||:|||||:|||||:  
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 15  
LOCUS BD263260 43 bp DNA linear PAT 17-JUL-2003  
DEFINITION Compositions and methods for use in recombinational cloning of nucleic acids.  
ACCESSION BD263260  
VERSION BD263260.1 GI:33073028  
KEYWORDS JP 2002537790-A/38.  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 43)  
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.  
TITLE Compositions and methods for use in recombinational cloning of nucleic acids  
JOURNAL Patent: JP 2002537790-A 38 12-NOV-2002;  
JOURNAL INVITROGEN CORP  
COMMENT OS Artificial Sequence  
PN JP 2002537790-A/38  
PD 12-NOV-2002



PF 02-MAR-2000 JP 2000602252  
 PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR  
 28-MAY-1999 US 60/136744  
 PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC  
 C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC  
 00, C12N5/00  
 CC attr2

Location/Qualifiers  
 FH Key 1..43  
 FT source /organism='Artificial Sequence'.  
 Location/Qualifiers  
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 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

FEATURES  
 source

ORIGIN

Query Match 83.2%; Score 20.8; DB 6; Length 43;  
 Best Local Similarity 80.0%; Pred. No. 8.4;  
 Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25  
 |||||:||||:||||:||||:  
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Search completed: November 16, 2004, 06:01:00  
 Job time : 709.5 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds  
(without alignments)  
782.095 Million cell updates/sec

Title: US-10-820-133-3

Perfect score: 25

Sequence: 1 gttcagctttcttactnaactsgb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
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5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
7: geneseqn2002bs.\*  
8: geneseqn2003as.\*  
9: geneseqn2003bs.\*  
10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	88.0	25	2	AAT48212
2	22	88.0	25	2	AAX78937
3	22	88.0	25	4	AAC87868
4	22	88.0	25	4	AAX78937
5	22	88.0	25	4	AAD14431
6	22	88.0	25	5	AAS14782
7	22	88.0	25	8	ABT16623
8	22	88.0	25	9	ACD28278
9	22	88.0	25	9	ACD28478
10	22	88.0	25	9	ADA38164
11	22	88.0	25	10	AAD60560
12	22	88.0	25	10	ACC44652
13	22	88.0	25	12	ADL93418
14	21.2	84.8	25	2	AAX78937
15	20.8	83.2	25	2	AAT48219
16	20.8	83.2	25	2	AAX78944
17	20.8	83.2	25	4	AAC87875
18	20.8	83.2	25	4	AAX78944
19	20.8	83.2	25	4	AAD14438
20	20.8	83.2	25	6	AQ82122
21	20.8	83.2	25	8	ABT16629

22	20.8	83.2	25	9	ACD28285	Acd28285 Nucleic a
23	20.8	83.2	25	9	ACD28485	Acd28485 Nucleic a
24	20.8	83.2	25	9	ADA38171	Ad38171 DNA of a
25	20.8	83.2	25	10	AAD60567	Aad60567 Core regi
26	20.8	83.2	25	10	ACC44659	Acc44659 Recombina
27	20.8	83.2	25	12	ADL93425	Adl93425 Recombina
28	20.8	83.2	25	12	AAS5546	Aas5546 att site
c	20.8	83.2	43	3	AAS06218	Aas06218 PCR prime
c	20.8	83.2	43	4	AAS06218	Aas06218 PCR prime
30	20.4	81.6	25	2	AAX78945	Aax78945 Oligonuc1
31	20.4	81.6	25	4	AAS06185	Aas06185 Phage-lam
32	20.4	81.6	25	10	ABZ58738	Abz58738 Att site
33	20.4	81.6	25	10	ACC59582	Acc59582 Nucleic a
34	20.4	81.6	25	12	ADJ46356	Adj46356 Wild type
35	20.4	81.6	25	12	ADO6650	Ado6650 att recom
c	20.4	81.6	25	12	ADQ48458	Adq48458 Bacterioph
37	20.4	81.6	37	12	ADH48079	Adh48079 Alpha-H-a
38	20.4	81.6	102	3	AAC55509	Aac55509 Destinati
39	20.4	81.6	102	3	AAC55512	Aac55512 Destinati
40	20.4	81.6	135	3	AAC55385	Aac55385 Recombina
41	20.4	81.6	153	3	AAC55506	Aac55506 Destinati
42	20.4	81.6	158	10	ADF42425	Adf42425 AtrR2 nuc
43	20.4	81.6	204	3	AAC55463	Aac55463 Destinati
44	20.4	81.6	1846	6	AAD44626	Aad44626 Gateway t
45	20.4	81.6	4554	3	AAC55541	Aac55541 attr read

## ALIGNMENTS

RESULT 1  
AAT48212

ID AAT48212 standard; DNA; 25 BP.

XX AC AAT48212;

DT 20-OCT-1997 (first entry)

XX M-attr core region.

DE att recombination site; core region; mutation; enhance; recombination;  
KW vector; subcloning; regulation; exchange; ss.

XX Synthetic.

XX WO9640724-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010082.

XX 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
XX using recombinant proteins and engineered recombination sites in vitro or  
XX in vivo.

XX Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The  
XX core region has at least one engineered mutation that enhances  
XX recombination in vitro in the formation of a Cointegrate or Product DNA.  
XX These core regions can be incorporated into novel vector donor DNA  
XX molecules. The nucleic acids, vectors and methods of the invention are  
XX used to obtain chimeric nucleic acid using recombination proteins and  
XX engineered recombination sites in vitro or in vivo. The improved  
XX specificity, speed and yields of the invention facilitates DNA or RNA  
XX subcloning, regulation or exchange useful for any related purpose, e.g.

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
CC or modification of transcribed, replicated, isolated or genomic DNA or  
CC RNA

XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match 88.0%; Score 22; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.86;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTKTRTACNAACTSGB 25  
|||||  
Db 1 GTTCAGCTTCTKTRTACNAACTSGB 25

## RESULT 2

AAx78937

ID AAX78937 standard; DNA; 25 BP.

XX

AC AAX78937;

XX 17-AUG-1999 (first entry)

XX Oligonucleotide #3 for recombination and cloning method.

XX Cloning; donor; recombination site; vector; chimeric; ss.

XX Synthetic.

XX WO9921977-A1.

XX 06-MAY-1999.

XX 26-OCT-1998; 98WO-US022589.

XX 24-OCT-1997; 97US-0065930P.

XX 23-OCT-1998; 98US-00177387.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Fox DK;

XX WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

XX Disclosure; Page 159; 195pp; English.

XX The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecules (IDMs) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMs) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more site-specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMs, thereby producing one or more desired product molecules (PMs). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention

XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;  
Query Match 88.0%; Score 22; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.86;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTKTRTACNAACTSGB 25  
|||||  
Db 1 GTTCAGCTTCTKTRTACNAACTSGB 25

## RESULT 3

AAC87868

ID AAC87868 standard; DNA; 25 BP.

XX

AC AAC87868;

XX 02-MAR-2001 (first entry)

XX Escherichia coli core region recombinant site m-attr SEQ ID NO:3.

XX Core region; recombination site; cloning; chimeric DNA; characteristic; mutation; att site; lox site; ss.

XX Escherichia coli.

XX US6143557-A.

XX 07-NOV-2000.

XX 20-JAN-1999; 99US-00233493.

XX 07-JUN-1995; 95US-00486139.

XX 07-JUN-1996; 96US-00663002.

XX 12-JAN-1998; 98US-00005476.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Brasch MA, Hartley JL;

XX WPI; 2001-049004/06.

XX Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered mutation.

XX Claim 1; Col 18; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site or avoids hairpin formation, the recombination site being an att or lox site; (2) an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a mutation that enhances recombination specificity; (3) vectors (IV) comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in engineering a core region of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and less labour intensive

XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match 88.0%; Score 22; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.86;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTKTRTACNAACTSGB 25  
|||||  
Db 1 GTTCAGCTTCTKTRTACNAACTSGB 25

## RESULT 4

AAF55737

ID AAF55737 standard; DNA; 25 BP.

XX

AC AAF55737;

```

XX 12-APR-2001 (first entry)
DT Recombination site m-attR.
DE Recombination site; cloning; m-att; ss.
XX Unidentified.
XX US6171861-B1.
XX 09-JAN-2001.
XX 12-JAN-1998; 98US-00005476.
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host.
XX Claim 24; Col 46; 73pp; English.
XX The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule, and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
CC invention
XX
SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;
Query Match 88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25
RESULT 5
AADI4431
ID AADI4431 standard; DNA; 25 BP.
XX AADI4431;
AC AADI4431;
XX 01-NOV-2001 (first entry)
DT Recombination site m-attR DNA.
XX Recombination site; copy number; replicon; recombinatorial cloning;
XX m-attR; ds.
XX Unidentified.
XX US6270969-B1.
XX 07-AUG-2001.
XX
XX 20-JAN-1999; 99US-00233492.
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX (INVI-) INVITROGEN CORP.
XX Hartley JL, Brasch MA;
XX WPI; 2001-488248/53.
XX Methods for apposing nucleic acids comprising an expression signal and a
PT gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under conditions
PT for recombination.
XX Claim 14; Col 18; 76pp; English.
XX The invention relates to a method for apposing an expression signal and a
CC gene or partial gene, using recombinatorial cloning. The method incubates
CC nucleic acids comprising the expression signal and the gene/partial gene
CC in the presence of a recombination protein under conditions sufficient to
CC cause recombination and therefore appose the expression signal and the
CC gene or partial gene. The methods are useful for apposing an expression
CC signal and a gene or partial gene using recombinatorial cloning. The
CC methods are also useful for changing vectors, constructing genes for
CC fusion proteins, changing copy number, changing replicons, cloning into
CC phages, and cloning e.g., PCR products (with an attB site at one end and
CC a loxP site at the other end), genomic DNAs, and cDNAs. The methods are
CC highly specific, rapid, and less labour intensive than prior art methods.
CC The present sequence is a recombination site useful for recombination
CC cloning
XX
SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;
Query Match 88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25
RESULT 6
AASI4782
ID AASI4782 standard; DNA; 25 BP.
XX AASI4782;
AC AASI4782;
XX 27-FEB-2002 (first entry)
DT Lambda phage Int recombinase site core region DNA sequence m-attR.
XX Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine;
XX syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour;
XX recombinase; tumour-specific promoter; hypoxic response element; HRE; ss;
XX tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer;
XX cytostatic; gene therapy; Int recombinase site core region; m-attR;
XX excisive recombination.
XX Bacteriophage lambda.
XX WO200174861-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US010250.
XX 31-MAR-2000; 2000US-0193977P.
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX

```

PI Vile RG, Harrington K, Murphy S, Bateman A;  
 XX WPI; 2001-656985/75.  
 XX Recombinant nucleic acid vector for reducing tumor size, has expression  
 PT cassette comprises a promoter linked to nucleic acid sequence encoding a  
 PT syncytium-inducing polypeptide and flanked on either side by recombinase.  
 XX  
 PS Disclosure; Page 42; 84pp; English.  
 XX The invention relates to a recombinant nucleic acid vector comprising a  
 CC first expression cassette, comprising a first promoter operably linked to  
 CC a nucleic acid sequence encoding a syncytium-inducing polypeptide (such  
 CC as a fusogenic membrane glycoprotein) and flanked on either side by a  
 CC sequence recognised by a recombinase, and/or a second expression cassette  
 CC comprising a tumour-specific promoter operably linked to a nucleic acid  
 CC sequence encoding a recombinase. The nucleic acid of the first expression  
 CC cassette may be linked to a hypoxic response element (HRE), the second  
 CC expression cassette may contain a promoter linked to a nucleic acid  
 CC encoding a cytokine, and a third cassette may contain a tumour specific  
 CC promoter linked to the nucleic acid encoding the recombinase. The tumour  
 CC specific promoter is, for example, a carcinoembryonic antigen (CEA)  
 CC promoter or a tyrosinase promoter and the recombinase is, for example,  
 CC Cre recombinase or FLP recombinase. The invention is useful for reducing  
 CC tumour size by administering the compositions as retroviral vectors, or  
 CC in a cell containing the vector, to an individual in need of treatment  
 CC for a disease caused by malignant cells. This sequence represents an Int  
 CC recombinase site core region m-attr, required for excisive recombination  
 XX  
 SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;  
 Query Match 88.0%; Score 22; DB 5; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.96;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTTCAGCTTCTCKRTACNAACTSGB 25  
 DB 1 GTTCAGCTTCTCKRTACNAACTSGB 25  
 RESULT 7  
 ABT16623  
 ID ABT16623 standard; DNA; 25 BP.  
 XX  
 AC ABT16623;  
 XX  
 DT 03-APR-2003 (first entry)  
 XX  
 DE Artificial plant chromosome related oligo SEQ ID No 35.  
 XX  
 KW Plant artificial chromosome; PAC; transgenic plant; vaccine;  
 KW blood factor; herbicide; stress; agronomical; nutrient quality;  
 KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;  
 KW ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200296923-A1.  
 XX  
 XX 05-DEC-2002.  
 PD  
 XX 30-MAY-2002; 2002WO-US017451.  
 XX  
 XX 30-MAY-2001; 2001US-0294687P.  
 PR  
 PR 04-JUN-2001; 2001US-0296329P.  
 XX  
 XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.  
 PA (AGRI-) AGRISOMA INC.  
 XX  
 XX Perez C, Fabijanski SF, Perkins E;  
 PI  
 XX WPI; 2003-140436/13.  
 DR  
 XX

PT Producing artificial chromosome by introducing a nucleic acid into plant  
 PT cell, selecting artificial chromosome that has one or more repeat regions  
 PT with equivalent amounts of euchromatic and heterochromatic nucleic acids.  
 XX  
 PS Disclosure; Page 261; 269pp; English.  
 XX The invention relates to a novel method for producing plant artificial  
 CC chromosomes. The invention also relates to methods for targeting  
 CC insertion of heterologous DNA into plant artificial chromosomes, methods  
 CC for delivery of plant chromosomes to selected cells and tissues. The  
 CC isolated plant artificial chromosome (PAC) is useful for producing a  
 CC transgenic plant, which involves introducing the PAC into a plant cell.  
 CC The PAC comprises a heterologous nucleic acid encoding a gene product  
 CC such as enzymes, antisense RNA, rDNA, structural proteins, marker  
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and  
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,  
 CC cytokines, growth factors, antibodies, or a product that provides for  
 CC resistance to diseases, insects, herbicides, or stress in a plant. The  
 CC heterologous nucleic acid optionally encodes a product that provides an  
 CC agronomically important trait in the plant, e.g. a product that alters  
 CC nutrient use and/or improves the nutrient quality of the plant. The  
 CC heterologous nucleic acid is contained within a bacterial artificial  
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This  
 CC polynucleotide sequence represents an oligo relating to the method for  
 CC producing plant artificial chromosomes of the invention  
 XX  
 SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;  
 Query Match 88.0%; Score 22; DB 8; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.86;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTTCAGCTTCTCKRTACNAACTSGB 25  
 DB 1 GTTCAGCTTCTCKRTACNAACTSGB 25  
 RESULT 8  
 ACD28278  
 ID ACD28278 standard; DNA; 25 BP.  
 XX  
 AC ACD28278;  
 XX  
 DT 02-OCT-2003 (first entry)  
 XX  
 DE Nucleic acid core region m-attr.  
 XX  
 KW Core region; ds; vector donor DNA; flanking recombination site; m-attr.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003064515-A1.  
 XX  
 PD 03-APR-2003.  
 XX  
 XX 30-JAN-2002; 2002US-00058291.  
 PF  
 XX 07-JUN-1995; 95US-00486139.  
 PR  
 PR 07-JUN-1996; 96US-00663002.  
 PR  
 PR 20-JAN-1999; 99US-00233493.  
 PR  
 PR 02-NOV-1999; 99US-00432085.  
 XX  
 XX (HART/) HARTLEY J L.  
 PA (BRAS/) BRASCH M A.  
 XX  
 PI Hartley JL, Brasch MA;  
 XX  
 XX WPI; 2003-540791/51.  
 DR  
 XX New Vector Donor DNA molecule for recombinational cloning using  
 PT engineered recombination sites, comprises first and second DNA segments  
 PT that do not recombine with each other and that contain a Selectable  
 PT marker.

XX Claim 14; Page 25; 71pp; English.

XX The invention relates to a vector donor DNA molecule comprising a first

CC DNA segment and a second DNA segment containing at least one selectable

CC marker. The first and second segments are separated either by, in a

CC circular vector donor, a first and a second recombination site, or in a

CC linear vector donor, at least a first recombination site, where each pair

CC of flanking recombination sites are engineered and do not recombine with

CC each other. The nucleic acid molecule, vectors and methods are useful for

CC moving or exchanging segments of DNA molecules using engineered

CC recombination sites and recombination proteins to provide chimeric DNA

CC molecules that have the desired characteristic(s) and/or DNA segment(s).

CC The present sequence represents the nucleic acid core region m-attr

XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

SQ Query Match 88.0%; Score 22; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.86;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25

Db 1 GTTCAGCTTCTCKTRTACNAACTSGB 25

RESULT 9

ACD28478

ID ACD28478 standard; DNA; 25 BP.

XX AC

AC ACD28478;

DT 09-OCT-2003 (first entry)

XX DE

XX Nucleic acid core sequence m-attr.

XX Nucleic acid core; m-attr; cointegrate DNA; flanking recombination site;

XX ds.

XX Synthetic.

XX US2003068799-A1.

XX 10-APR-2003.

XX 06-JUN-2002; 2002US-00162879.

XX 07-JUN-1995; 95US-00486139.

XX 07-JUN-1996; 96US-00563002.

XX 20-JAN-1999; 99US-00233493.

XX 02-NOV-1999; 99US-00432085.

XX (INVI-) INVITROGEN CORP.

XX Hartley JL, Brasch MA;

XX WPI; 2003-540884/51.

XX Making Cointegrate DNA molecule, by combining recombination sites

PT flanking the desired DNA segment in insert donor DNA, with the

PT recombination sites of vector donor DNA, using site specific

PT recombination protein.

XX Claim 14; Page 25; 71pp; English.

XX The invention relates to a method of making a cointegrate DNA molecule.

CC The method is useful for making a cointegrate DNA molecule. The method is

CC useful for a variety of DNA exchanges, such as subcloning of DNA, in

CC vitro or in vivo. The method enables efficient and specific recombination

CC of DNA segments using recombination proteins. The method is highly

CC specific, rapid and less labour intensive. The improved specificity,

CC yield and speed of the method facilitates DNA or RNA subcloning,

CC regulation and exchange useful for other related purposes. Since single

CC molecules of the recombinations product can be introduced into a

CC biological host, propagation of the desired product DNA in the absence of

CC other DNA molecules is more readily realised. Reaction conditions can be

CC freely adjusted in vitro to optimise enzyme activities. The present

CC sequence represents the nucleic acid core sequence m-attr

XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

SQ Query Match 88.0%; Score 22; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.86;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25

Db 1 GTTCAGCTTCTCKTRTACNAACTSGB 25

RESULT 10

ADA38164

ID ADA38164 standard; DNA; 25 BP.

XX AC

AC ADA38164;

DT 20-NOV-2003 (first entry)

XX DE

XX m-attr DNA sequence indicating generic core region of an attR site.

XX engineered recombination site; cloning; recombinase; subcloning; attB;

XX attP; attL; attR; selectable marker; cointegrate; m-attr; ds.

XX Synthetic.

XX US2003054552-A1.

XX 20-MAR-2003.

XX 30-JAN-2002; 2002US-00058292.

XX 07-JUN-1995; 95US-00486139.

XX 07-JUN-1996; 96US-00563002.

XX 20-JAN-1999; 99US-00233493.

XX 02-NOV-1999; 99US-00432085.

XX (HART/) HARTLEY J L.

XX (BRAS/) BRASCH M A.

XX Hartley JL, Brasch MA;

XX WPI; 2003-585168/55.

XX New Vector Donor DNA molecule, useful for recombinational cloning

PT purposes, comprises a first and a second DNA segment that contains a

PT selectable marker and is separated by a pair of flanking, engineered

PT recombination sites.

XX Claim 14; Page 26; 72pp; English.

XX This invention relates to novel DNA and vectors having engineered

CC recombination sites for use in a cloning method that enables efficient

CC and specific recombination of DNA segments using recombination proteins

CC including recombinases. As such, it provides a method for obtaining

CC chimeric nucleic acids with the desired characteristics, facilitating DNA

CC or RNA subcloning, regulation and/or exchange. The recombination site is

CC derived from attB attP, attL or attR, where the att site is att1, att2 or

CC att3. Engineered mutations of the att sites (either one or multiple

CC mutations) can enhance specificity or efficiency of the recombination

CC reaction and the properties of the product DNA molecules. Accordingly,

CC the present invention describes a nucleic acid molecule comprising at

CC least one DNA segment having at least two engineered recombination sites

CC flanking a selectable marker and/or a desired DNA segment. Furthermore,

CC at least one of the engineered sites must enhance recombination in vitro

CC to form a cointegrate or product DNA molecule. This oligonucleotide

CC sequence is m-attr, a generic DNA sequence indicating the core region of

```

CC an attr recombination site of the invention.
SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match      88.0%; Score 22; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCTKTRTACNAACTSGB 25

RESULT 11
AAD60560
ID AAD60560 standard; DNA; 25 BP.
XX
AC AAD60560;
XX
DT 18-DEC-2003 (first entry)
XX
DE Core region DNA, m-attr.
XX
KW Recombinational cloning; DNA exchange; core region; ds.
XX
OS Unidentified.
XX
PN US2003100110-A1.
XX
PD 29-MAY-2003.
XX
PF 02-NOV-1999; 99US-00432085.
XX
PR 07-JUN-1995; 95US-00486139.
XX
PR 07-JUN-1996; 96US-00663002.
XX
PR 20-JAN-1999; 99US-00233493.
XX
PA (HART/) HARTLEY J L.
PA (BRAS/) BRASCH M A.
XX
PI Hartley JL, Brasch MA;
XX
DR WPI; 2003-730143/69.
XX
New Vector Donor DNA molecule for recombinational cloning using
PT engineered recombination sites, comprises first and second DNA segments
PT that do not recombine with each other and that contain a Selectable
PT marker.
XX
PS Claim 14; Page 25; 71pp; English.
XX
The invention relates to a vector donor DNA molecule which comprises
CC first and second DNA segments that do not recombine with each other and
CC that contain a selectable marker. The invention also relates to a method
CC for recombinational cloning using engineered recombination sites. The
CC invention is useful for moving or exchanging segments of DNA molecules
CC using engineered recombination sites and recombination proteins to
CC provide chimeric DNA molecules that have the desired characteristic(s)
CC and/or DNA segment(s). The present sequence is a core region DNA. This
CC sequence is used to illustrate the method of the invention
XX
SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match      88.0%; Score 22; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCTKTRTACNAACTSGB 25

RESULT 12

```

```

ACC44652
ID ACC44652 standard; DNA; 25 BP.
XX
AC ACC44652;
XX
DT 29-MAY-2003 (first entry)
XX
DE Recombination site related oligonucleotide SEQ ID NO:43.
XX
KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
KW platform artificial chromosome expression system; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200297059-A2.
XX
PD 05-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-US017452.
XX
PR 30-MAY-2001; 2001US-0294758P.
XX
PR 21-MAR-2002; 2002US-0366891P.
XX
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX
PI Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
PI Stewart S, Shellard J;
XX
DR WPI; 2003-140461/13.
XX
Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
PT interest.
XX
PS Claim 43; Page 143; 272pp; English.
XX
The present invention describes a eukaryotic chromosome (I) comprising
CC one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (i) a platform artificial chromosome
CC expression system (ACes) (II) comprising several sites that participate
CC in recombinase catalysed recombination; and (2) a method (M1) for
CC introducing a heterologous nucleic acid into a platform artificial
CC chromosome. (I) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an ACes. (II) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection,
CC by a carrier system, microinjection, microcell fusion, electroporation,
CC microprojectile bombardment or direct DNA transfer into an embryonic
CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
CC nucleic acid that encodes a therapeutic product which is useful for
CC making a library of ACes comprising random portions of a genome. ACC44612
CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match      88.0%; Score 22; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCTKTRTACNAACTSGB 25

RESULT 13
ADL93418
ID ADL93418 standard; DNA; 25 BP.
XX

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds  
(without alignments)  
494.978 Million cell updates/sec

Title: US-10-820-133-3

Perfect score: 25

Sequence: 1 gttcagtttcttactnaactsgb 25

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
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5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	88.0	25	3	US-09-233-493-3
2	22	88.0	25	3	US-09-005-476-3
3	22	88.0	25	3	US-09-233-492-3
4	22	88.0	25	3	US-09-296-280-3
5	22	88.0	25	4	US-09-498-074-3
6	22	88.0	25	4	US-09-498-074-3
7	22	88.0	25	5	PCT-US96-10082A-3
8	21.2	84.8	25	3	US-09-296-280-42
9	20.8	83.2	25	3	US-09-233-493-10
10	20.8	83.2	25	3	US-09-005-476-10
11	20.8	83.2	25	3	US-09-233-492-10
12	20.8	83.2	25	3	US-09-296-280-10
13	20.8	83.2	25	4	US-09-498-074-10
14	20.8	83.2	25	4	US-09-498-074-10
15	20.8	83.2	25	5	PCT-US96-10082A-10
16	20.4	81.6	25	3	US-09-296-280-11
17	20	80.0	25	3	US-09-233-493-5
18	20	80.0	25	3	US-09-005-476-5
19	20	80.0	25	3	US-09-233-492-5
20	20	80.0	25	3	US-09-296-280-5
21	20	80.0	25	4	US-09-498-074-5
22	20	80.0	25	4	US-09-498-074-5
23	20	80.0	25	5	PCT-US96-10082A-5
24	19.6	78.4	25	3	US-09-233-493-1
25	19.6	78.4	25	3	US-09-005-476-1
26	19.6	78.4	25	3	US-09-233-492-1
27	19.6	78.4	25	3	US-09-296-280-1

28 19.6 78.4 25 4 US-09-498-074-1 Sequence 1, Appli  
29 19.6 78.4 25 4 US-09-498-074-1 Sequence 1, Appli  
30 19.6 78.4 25 5 PCT-US96-10082A-1 Sequence 1, Appli  
31 19.2 76.8 25 3 US-09-233-493-9 Sequence 9, Appli  
32 19.2 76.8 25 3 US-09-233-493-11 Sequence 11, Appli  
33 19.2 76.8 25 3 US-09-233-493-16 Sequence 16, Appli  
34 19.2 76.8 25 3 US-09-005-476-9 Sequence 9, Appli  
35 19.2 76.8 25 3 US-09-005-476-11 Sequence 11, Appli  
36 19.2 76.8 25 3 US-09-005-476-16 Sequence 16, Appli  
37 19.2 76.8 25 3 US-09-233-492-9 Sequence 9, Appli  
38 19.2 76.8 25 3 US-09-233-492-11 Sequence 11, Appli  
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40 19.2 76.8 25 3 US-09-296-280-9 Sequence 9, Appli  
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42 19.2 76.8 25 3 US-09-296-280-39 Sequence 39, Appli  
43 19.2 76.8 25 4 US-09-498-074-9 Sequence 9, Appli  
44 19.2 76.8 25 4 US-09-498-074-11 Sequence 11, Appli  
45 19.2 76.8 25 4 US-09-498-074-16 Sequence 16, Appli

#### ALIGNMENTS

RESULT 1  
US-09-233-493-3  
; Sequence 3, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
US-09-233-493-3

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Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSG 25
    |||||
Db 1 GTTCAGCTTCTCKTRTACNAACTSG 25

RESULT 2
US-09-005-476-3
; Sequence 3, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-3

Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSG 25
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Db 1 GTTCAGCTTCTCKTRTACNAACTSG 25

RESULT 3
US-09-233-492-3
; Sequence 3, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-492-3

Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSG 25
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Db 1 GTTCAGCTTCTCKTRTACNAACTSG 25

RESULT 4
US-09-296-280-3
; Sequence 3, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-296-280-3
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Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCKTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTACNAACTSGB 25

RESULT 5
US-09-498-074-3
; Sequence 3, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; REcombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-498-074-3

Query Match      88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCKTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTACNAACTSGB 25

RESULT 6
US-09-498-074-3
; Sequence 3, Application US/09498074
; Patent No. 6720140
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; REcombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-498-074-3

Query Match      88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCKTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTACNAACTSGB 25

RESULT 7
PCT-US96-10082A-3
; Sequence 3, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; REcombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-498-074-3
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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: 04-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-498-074-3

Query Match      88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCKTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTACNAACTSGB 25

RESULT 7
PCT-US96-10082A-3
; Sequence 3, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; REcombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-498-074-3
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APPLICATION NUMBER: US/09/005,476  
FILING DATE: herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
US-09-005-476-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;  
Best Local Similarity 80.0%; Pred. No. 0.28;  
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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|||||:|||||:|||||:|||||:  
Db 1 GTTCAGCTTCTTGTACAAACTTGT 25

RESULT 11  
US-09-233-492-10  
Sequence 10, Application US/09233492  
Patent No. 6270969  
GENERAL INFORMATION:  
APPLICANT: Hartley, James L.  
APPLICANT: Brasch, Michael A.  
TITLE OF INVENTION: Recombinational Cloning Using Engineered  
TITLE OF INVENTION: Recombination Sites  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
STREET: 1100 New York Ave., N. W. Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/233,492  
FILING DATE: 20-JAN-1999

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
US-09-233-492-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;  
Best Local Similarity 80.0%; Pred. No. 0.28;  
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTKTRTACNAACTSGB 25  
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Db 1 GTTCAGCTTCTTGTACAAACTTGT 25

RESULT 12  
US-09-296-280-10  
Sequence 10, Application US/09296280  
Patent No. 6277608  
GENERAL INFORMATION:  
APPLICANT: Hartley, James L.  
APPLICANT: Brasch, Michael A.  
APPLICANT: Temple, Gary F.  
APPLICANT: Fox, Donna K.  
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
TITLE OF INVENTION: Recombination Sites  
FILE REFERENCE: 0942.2850007  
CURRENT APPLICATION NUMBER: US/09/296,280  
EARLIER FILING DATE: 1999-04-22  
EARLIER APPLICATION NUMBER: US 09/177,387  
EARLIER FILING DATE: 1998-10-23  
EARLIER APPLICATION NUMBER: US 60/065,930  
EARLIER FILING DATE: 1997-10-24  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: recombination  
US-09-296-280-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;  
Best Local Similarity 80.0%; Pred. No. 0.28;  
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTCTTGTACAAACTTGT 25

RESULT 13  
US-09-498-074-10  
Sequence 10, Application US/09498074  
Patent No. 6534264  
GENERAL INFORMATION:  
APPLICANT: Hartley, James L.  
APPLICANT: Brasch, Michael A.  
TITLE OF INVENTION: Recombinational Cloning Using Engineered  
TITLE OF INVENTION: Recombination Sites  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
STREET: 1100 New York Ave., N. W. Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,074  
FILING DATE: (Herewith)  
CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-10

Query Match      83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTCTGTACAACTTGT 25

RESULT 14
US-09-498-074-10
; Sequence 10, Application US/09498074
; Patent No. 6720140
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
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; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: both
; TOPOLOGY: both
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US-09-498-074-10

Query Match      83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTCTGTACAACTTGT 25

RESULT 15
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; Sequence 10, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
PCT-US96-10082A-10

Query Match      83.2%; Score 20.8; DB 5; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCTGTACAACTTGT 25

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Job time : 35.9 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 ; Search time 314 Seconds  
(without alignments)  
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Title: US-10-820-133-3

Perfect score: 25

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

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Minimum DB seq length: 0

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Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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3	22	88.0	25	9	US-09-907-900-3
4	22	88.0	25	9	US-09-907-719-3
5	22	88.0	25	10	US-09-432-085-3
6	22	88.0	25	10	US-09-985-448-3
7	22	88.0	25	14	US-10-058-292-3
8	22	88.0	25	14	US-10-058-291-3
9	22	88.0	25	14	US-10-162-879-3
10	22	88.0	25	15	US-10-161-403-43
11	22	88.0	25	15	US-10-300-892-3
12	22	88.0	25	16	US-10-680-316-3

13	22	88.0	25	17	US-10-815-730-3	Sequence 3, Appli
14	22	88.0	25	17	US-10-820-133-3	Sequence 3, Appli
15	22	88.0	25	18	US-10-161-408-35	Sequence 35, Appli
16	22	88.0	25	18	US-10-796-868A-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1

US-09-855-797A-3  
; Sequence 3, Application US/09855797A  
; Patent No. US20020094574A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850008  
; CURRENT APPLICATION NUMBER: US/09/855.797A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/296,281  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-855-797A-3

Query Match 88.0%; Score 22; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

## RESULT 2

US-09-822-634-4  
; Sequence 4, Application US/09822634  
; Patent No. US20020150556A1  
; GENERAL INFORMATION:  
; APPLICANT: Vile, Richard G.  
; APPLICANT: Harrington, Kevin  
; APPLICANT: Bateman, Andrew  
; APPLICANT: Murphy, Steven  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE  
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY  
; FILE REFERENCE: 07039-289001  
; CURRENT APPLICATION NUMBER: US/09/822,634  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/193,977  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated vector sequence  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(25)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-822-634-4

Query Match 88.0%; Score 22; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCKTRTACNAACTSGB 25  
|||||  
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

## RESULT 3

US-09-907-900-3  
; Sequence 3, Application US/09907900  
; Patent No. US20020172997A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.285004  
; CURRENT APPLICATION NUMBER: US/09/907,900  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-900-3

Query Match 88.0%; Score 22; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCKTRTACNAACTSGB 25  
|||||  
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

## RESULT 4

US-09-907-719-3  
; Sequence 3, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.285004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-719-3

Query Match 88.0%; Score 22; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCKTRTACNAACTSGB 25  
|||||  
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

## RESULT 5

US-09-432-085-3  
; Sequence 3, Application US/09432085  
; Publication No. US20030100110A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,085

Query Match 88.0%; Score 22; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.58;

Query Match 88.0%; Score 22; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.58;

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07-198
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 202-371-2600
    TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
    LENGTH: 25 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: both
    TOPOLOGY: both
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-058-292-3

Query Match      88.0%; Score 22; DB 14; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.56;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTCKTRTACNAACTSGB 25
        |||||||
Db       1 GTTCAGCTTTCKTRTACNAACTSGB 25

RESULT 8
US-10-058-291-3
; Sequence 3, Application US/10058291
; Publication No. US20030064515A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brasch, Michael A.
```

```
/
/
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ Recombination Sites
/
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA: US/10/058,291
/ APPLICATION NUMBER: US/10/058,291
/ FILING DATE: 30-Jan-2002
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/432,085
/ FILING DATE: 1999-11-02
/ APPLICATION NUMBER: 09/233,493
/ FILING DATE: 20-JAN-1999
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cDNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-058-291-3

Query Match 88.0%; Score 22; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTKTRTACNAACTSGB 25
| | | | | | | | | | | | | | | | |
Db 1 GTTCAGCTTCTKTRTACNAACTSGB 25

RESULT 9
US-10-162-879-3
; Sequence 3, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
/
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ Recombination Sites
/
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
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/
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/162,879
/ FILING DATE: 06-Jun-2002
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/432,085
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: 09/233,493
/ FILING DATE: 20-JAN-1999
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cDNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-162-879-3

Query Match 88.0%; Score 22; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTKTRTACNAACTSGB 25
| | | | | | | | | | | | | | | | |
Db 1 GTTCAGCTTCTKTRTACNAACTSGB 25

RESULT 10
US-10-161-403-43
; Sequence 43, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
/
/ TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
/ FILE REFERENCE: 24601-420
/ CURRENT APPLICATION NUMBER: US/10/161,403
/ CURRENT FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: 60/294,758
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: 60/366,891
/ PRIOR FILING DATE: 2002-03-21
/ NUMBER OF SEQ ID NOS: 129
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 43
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: m-attr
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: 18
/ OTHER INFORMATION: n is a o r g o r c o r t/u
US-10-161-403-43
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Query Match 88.0%; Score 22; DB 15; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25  
Db 1 GTTCAGCTTTCTKTRTACNAACTSGB 25

## RESULT 11

US-10-300-892-3  
; Sequence 3, Application US/10300892  
; Publication No. US20030175970A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/10/300,892  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US/09/907,719  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-10-300-892-3

Query Match 88.0%; Score 22; DB 15; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25  
Db 1 GTTCAGCTTTCTKTRTACNAACTSGB 25

## RESULT 12

US-10-680-316-3  
; Sequence 3, Application US/10680316  
; Publication No. US20040063207A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/10/680,316  
; CURRENT FILING DATE: 2003-10-08  
; PRIOR APPLICATION NUMBER: US/09/177,387A  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 25

; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-10-680-316-3

Query Match 88.0%; Score 22; DB 16; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25  
Db 1 GTTCAGCTTTCTKTRTACNAACTSGB 25

## RESULT 13

US-10-815-730-3  
; Sequence 3, Application US/10815730  
; Publication No. US20040171156A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/10/815,730  
; CURRENT FILING DATE: 2004-04-02  
; PRIOR APPLICATION NUMBER: US/09/177,387A  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-10-815-730-3

Query Match 88.0%; Score 22; DB 17; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25  
Db 1 GTTCAGCTTTCTKTRTACNAACTSGB 25

## RESULT 14

US-10-820-133-3  
; Sequence 3, Application US/10820133  
; Publication No. US20040171157A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/10/820,133  
; CURRENT FILING DATE: 2003-10-08  
; PRIOR APPLICATION NUMBER: US/09/177,387A  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 25

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/ FILE REFERENCE: 0942.2850004
/ CURRENT APPLICATION NUMBER: US/10/820,133
/ CURRENT FILING DATE: 2004-04-08
/ PRIOR APPLICATION NUMBER: US/09/177,387A
/ PRIOR FILING DATE: 1998-10-23
/ PRIOR APPLICATION NUMBER: US 60/065,930
/ PRIOR FILING DATE: 1997-10-24
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ NAME/KEY: OTHER
/ LOCATION: 18
/ OTHER INFORMATION: "n" may be any nucleotide
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: recombination
/ OTHER INFORMATION: products
US-10-820-133-3

Query Match      88.0%; Score 22; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCAGCTTCKTRTACNAACTSGB 25
        |||||
Db      1 GTTCAGCTTCKTRTACNAACTSGB 25

RESULT 15
US-10-161-408-35
/ Sequence 35, Application US/10161408
/ Publication No. US20040214290A1
/ GENERAL INFORMATION:
/ APPLICANT: Perez, Carl
/ APPLICANT: Fabijanski, Steven
/ APPLICANT: Perkins, Edward
/ TITLE OF INVENTION: Plant Artificial Chromosomes, Uses thereof, and Methods of Preparation
/ FILE REFERENCE: 24601-419
/ CURRENT APPLICATION NUMBER: US/10/161,408
/ CURRENT FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: US 60/294,687
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: US 60/296,329
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: m-atrr recognition sequence
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: 18
/ OTHER INFORMATION: n is a or g or c or t/u
US-10-161-408-35

Query Match      88.0%; Score 22; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCAGCTTCKTRTACNAACTSGB 25
        |||||
Db      1 GTTCAGCTTCKTRTACNAACTSGB 25

Search completed: November 16, 2004, 11:14:58
Job time : 314.1 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds  
(without alignments)  
594.643 Million cell updates/sec

Title: US-10-820-133-3

Perfect score: 25

Sequence: 1 gttcagtttcttctacnaactsgb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_ges1:\*

9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20.2	80.8	708	8	AQ990869 Rfc01706
C 2	20	80.0	829	9	CC863243 ND.L.10401
C 3	20	80.0	836	8	CC118013 ND.L.78N18
C 4	19	76.0	770	8	AQ991774 Rfc02039F
C 5	19	76.0	791	8	AQ991791 Rfc02368F
C 6	19	76.0	1161	7	CK162252 FGAS01484
C 7	18.8	75.2	321	2	BF086649 CM0-GN007
C 8	18.8	75.2	595	2	AW993039 RC2-BN003
C 9	18.8	75.2	635	7	CN484020 hw41b03.Y
C 10	18.8	75.2	672	8	AQ990864 Rfc01701
C 11	18.8	75.2	706	4	B1836912 603084230
C 12	18.8	75.2	714	5	BX359053 BX359053
C 13	18.8	75.2	752	4	BG620766 602617479
C 14	18.8	75.2	753	8	AQ990861 Rfc01698
C 15	18.8	75.2	797	4	BG427603 602497040
C 16	18.8	75.2	805	7	CR629462 DKFZp493K
C 17	18.8	75.2	808	8	AQ990388 Rfc01153
C 18	18.8	75.2	810	5	BQ216337 AGENCOURT
C 19	18.8	75.2	824	4	BG620383 602617507
C 20	18.8	75.2	831	5	BQ230007 AGENCOURT
C 21	18.8	75.2	852	4	BG401996 602466712
C 22	18.8	75.2	855	2	BE785867 601478671
C 23	18.8	75.2	856	2	BE893159 601437059
C 24	18.8	75.2	859	5	BX398237 BX398237

25	18.8	75.2	862	2	BE895530
26	18.8	75.2	908	4	B1546971 603190186
27	18.8	75.2	954	5	BQ893686
28	18.8	75.2	986	5	BX398580 BX398580
29	18.8	75.2	994	4	BM804936 AGENCOURT
30	18.8	75.2	1019	2	BE300319 600944384
31	18.4	73.6	94	7	CF652584 64-L02052
32	18.4	73.6	95	7	CF652701 71-L02052
33	18.4	73.6	127	9	CL308706
C 34	18.4	73.6	628	6	CL324539 StrFu537
C 35	18.2	72.8	402	9	CL604547 CH240_180
C 36	18.2	72.8	444	9	AG239085 Lotus cor
C 37	18.2	72.8	509	8	AQ165422 HS_3031_A
C 38	18.2	72.8	794	8	BO929333 RPi-2473
C 39	18.2	72.8	1000	5	BU60343 603501901
C 40	18.2	72.8	1770	9	AG081618 Pan trogl
C 41	18	72.0	613	8	AZ431189 IM0216C04
C 42	18	72.0	686	4	BJ606288 BJ606288
C 43	18	72.0	707	4	BJ588203 BJ588203
C 44	18	72.0	756	8	AQ991732 Rfc00380F
C 45	18	72.0	762	4	BJ611386 BJ611386

#### ALIGNMENTS

RESULT 1  
AQ990869/c

LOCUS  
DEFINITION

AQ990869 708 bp DNA linear GSS 14-AUG-2000  
Rfc01706 Photorhabdus luminescens strain W14 M13 library  
Photorhabdus luminescens genomic clone PLG01706, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

AQ990869 708 bp DNA linear GSS 14-AUG-2000  
Rfc01706 Photorhabdus luminescens strain W14 M13 library  
Photorhabdus luminescens genomic clone PLG01706, genomic survey sequence.  
AQ990869 GI:9649463  
GSS.  
Photorhabdus luminescens  
Photorhabdus luminescens  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Photorhabdus.  
1 (bases 1 to 708)  
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,  
Daborn, P.J., Bowen, D. and Blattner, F.R.  
A genomic sample sequence of the entomopathogenic bacterium  
Photorhabdus luminescens W14: potential implications for virulence  
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)  
20378633  
10919786  
Contact: ffrench-Constant RH  
Department of Biology and Biochemistry  
University of Bath  
South Building, Bath BA2 7AY, UK  
Tel: (44) 1225 826621  
Fax: (44) 1225 826779  
Email: bsarf@bath.ac.uk  
This is one of 2,122 random reads from the M13 library. For  
annotation of identified clones (BLASTX, BLASTN and mapping to B.  
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic  
Acids Res.  
Seq primer: M13 Forward  
Class: shotgun.  
Location/Qualifiers  
1. .708  
/organism="Photorhabdus luminescens"  
/mol\_type="genomic DNA"  
/strain="W14"  
/db\_xref="taxon:29488"  
/clone="PLG01706"  
/dev\_stage="primary phase variant"  
/clone\_lib="Photorhabdus luminescens strain W14 M13  
library"  
/note="Genomic DNA from strain W14 was size selected (1-2  
kb) and then cloned into M13 Janus."

FEATURES  
source

ORIGIN

```

Query Match      80.8%; Score 20.2; DB 8; Length 708;
Best Local Similarity 79.2%; Pred. No. 48;
Matches 19; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1  GTTCAGCTTTCTKTRTACNAACTSG 24
          ||||| :||| |||
Db      348 GTTCAGCTTTTATCTACTAATCG 325
          ||||| :||| |||

```

RESULT 2	
CC863243	
LOCUS	829 bp DNA linear GSS 24-JUL-2003
DEFINITION	NDL_104O15.SP6 Notre Dame Liverpool Aedes aegypti genomic clone notreDame Liverpool-104O15, genomic survey sequence.
ACCESSION	CC863243
VERSION	CC863243.1 GI:33223253
KEYWORDS	GSS.
SOURCE	Aedes aegypti (yellow fever mosquito)
ORGANISM	Aedes aegypti
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 829)  
Loftus,B., Shetty,J., Knudson,D. and Severson,D.  
BAC end sequencing of Aedes aegypti  
Unpublished (2003)  
Other GSSs: NDL.104O15.T7  
Contact: Brendan Loftus  
Department of Eukaryotic Genomics  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: enta@tigr.org  
Library was provided by David Severson  
Seq primer: SP6  
Clase: bac\_end

```

Class: BAC ends.
Location/Qualifiers
1. 829
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="NotreDame Liverpool-104015"
/clone_lib="Notre Dame Liverpool"
/note="Vector: pECBAC1, Site1: Hind III; The library was
prepared from whole body tissue of newly hatched 1st larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"

ORIGIN

Query Match 80.0%; Score 20; DB 9; Length 829;
Best Local Similarity 78.3%; Pred. No. 62;
Matches 18; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCAGCTTTCTKTRTACNAACTSGB 25
|||||:|||||:
Db 382 TCAGCTTTCGTATACCAACTCGT 404
|||||:|||||:

```

Stegomyia.  
1 (bases 1 to 836)  
AUTHORS Lofas, B., Shetty, J., Knudson, D. and Severson, D.  
TITLE BAC end sequencing of Aedes aegypti  
JOURNAL Unpublished (2003)  
COMMENT Other GSSS: NDL.78N18.SP6  
Contact: Brendan Loftus  
Department of Eukaryotic Genomics  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: enta@tigr.org  
Library was provided by David Severson  
Seg primer: T7  
Class: RAC ends

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Class: L1
FEATURES
  source
    Location/Qualifiers
      1..836
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        /mol_type="genomic DNA"
        /strain="Liverpool"
        /db_xref="taxon:7159"
        /clone="NDL.78N18"
        /clone_lib="Notre Dame Liverpool"
        /note="Vector: pGEBAC1; Site_1: Hind III; The library was
        prepared from whole body tissue of newly hatched L1 larvae
        by David Severson at the University of Notre Dame and
        Hongbin Zhang"

ORIGIN
  Query Match      80.0%; Score 20; DB 8; Length 836;
  Best Local Similarity 78.3%; Pred. No. 62;
  Matches 18; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCAGCTTTTCKTRTACNAACTSGE 25
         |||||:|||||:|||||:
Db      391 TCAGCTTTTGGTATACCAACTCGT 413
         |||||:|||||:|||||:

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RESULT 4	
AQ991774/c	
LOCUS	770 bp DNA linear GSS 14-AUG-2000
DEFINITION	Efc02039F Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone FLG02039F, genomic survey sequence.
ACCESSION	AQ991774
VERSION	AQ991774
KEYWORDS	AQ991774.1 GI:9650368
SOURCE	GSS.
ORGANISM	Photorhabdus luminescens Photorhabdus luminescens Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus

REFERENCE	1 (bases 1 to 770)
AUTHORS	french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Dabon,P.J., Bowen,D. and Blattner,F.R.
TITLE	A genomic sample sequence of the enteropathogenic bacterium Photobacterium luminescens w14: potential implications for virulence
JOURNAL	Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE	20378633
PubMed	10919786
COMMENT	Contact: french-Constant RH Department of Biology and Biochemistry University of Bath South Building, Bath BA2 7AY, UK Tel: (44) 1225 826621 Fax: (44) 1225 826779 Email: bsarfcbath.ac.uk This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BIASRX, BLASTN and mapping to E. coli M12 genome) please see french-Constant et al. 2000, Nucleic Acids Res. Seq primer: M13 Reverse Class: shotgun.



```

FEATURES
  source
    Location/Qualifiers
      1..770
        /organism="Photorhabdus luminescens"
        /mol_type="genomic DNA"
        /strain="W14"
        /db_xref="taxon:29488"
        /clones="PLG02039F"
        /dev_stages="primary phase variant"
        /clone_lib="Photorhabdus luminescens strain W14 M13 library"
        /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
  Query Match      76.0%; Score 19; DB 8; Length 770;
  Best Local Similarity 79.2%; Pred. No. 2e+02;
  Matches 19; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCKTRTACNAACTSG 24
    ||||| :|||
Db 59 GTTCAGCTTTTATACTACTTG 36

RESULT 5
AQ991791/c
LOCUS
DEFINITION
  Photorhabdus luminescens genomic clone PLG02368F, genomic survey
  sequence.
ACCESSION
  AQ991791
VERSION
  GSS
KEYWORDS
  GSS.
SOURCE
  Photorhabdus luminescens
  ORGANISM
    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
    Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (Bases 1 to 791)
  ffrrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL
  MEDLINE
  PUBMED
  10919786
COMMENT
  Contact: ffrrench-Constant RH
  Department of Biology and Biochemistry
  University of Bath
  South Building, Bath BA2 7AY, UK
  Tel: (44) 1225 826621
  Fax: (44) 1225 826779
  Email: bsarfc@bath.ac.uk
  This is one of a selected subset of flipped clones from the M13
  library. For annotation of identified clones (BLASTX, BLASTN and
  mapping to E. coli K12 genome) please see ffrrench-Constant et al.
  2000, Nucleic Acids Res.
  Seq primer: M13 Reverse
  Class: shotgun.
FEATURES
  source
    Location/Qualifiers
      1..791
        /organism="Photorhabdus luminescens"
        /mol_type="genomic DNA"
        /strain="W14"
        /db_xref="taxon:29488"
        /clones="PLG02368F"
        /dev_stages="primary phase variant"
        /clone_lib="Photorhabdus luminescens strain W14 M13 library"
        /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
  Query Match      76.0%; Score 19; DB 8; Length 791;
  Best Local Similarity 79.2%; Pred. No. 2e+02;

FEATURES
  source
    Location/Qualifiers
      1..1161
        /organism="Triticum aestivum"
        /mol_type="mRNA"
        /db_xref="taxon:4565"
        /clone_lib="Triticum aestivum FGAS: Library 4 Gate 8"
        /note="Organ: Crown and leaf; Vector: pCMV.SPORI6;
        Conditions for growth: Seeds were germinated in a
        water-saturated mix (50% black earth and 50% ProMix) in a
        growth chamber for 7 days under an irradiance of 200 mmol
        m-2 sec-1. The temperature was maintained at 20 degrees C
        with a 15-hr photoperiod under a relative humidity of 70%.
        After this period watering of plants was stopped. Four
        time points were sampled during a two week period; the
        first after wilting was observed and the last, two weeks
        later, consisted of live crown and leaf tissue (leaf
        tissue that was yellow was not included in sampled
        material). First strand synthesis in this library was done
        in the presence of methylated dCTP thereby protecting from
        internal cleavage with NotI."

ORIGIN
  Query Match      76.0%; Score 19; DB 7; Length 1161;
  Best Local Similarity 77.3%; Pred. No. 2.le+02;
  Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCKTRTACNAACTSGB 25
    ||||| :|||
Db 553 CAGCTTTCTGTACAACTGGT 574

RESULT 7

```



```

Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 41 row: b column: 03
Seq primer: M13RP1 reverse primer (ABI).

FEATURES
    source
        1. 635
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="hw41b03"
            /cell_type="pericytes"
            /dev_stage="Adult"
            /lab_host="EMPH10B"
            /clone_lib="Human primary human ocular pericytes.
            Unamplified (hw)"
            /note="Organ: Eye; Vector: pSPORT1; RNA was extracted from
            primary human pericytes in culture. A directionally cloned
            cDNA library in the pSPORT1 vector (Invitrogen) was
            constructed at Bioserve Biotechnology (Laurel MD)
            essentially following the protocols of the Superscript
            Plasmid System full details of which are contained in the
            manufacturer's instruction manual
            (http://www.lifetech.com/). First strand synthesis was
            carried out using a Not I primer-adaptor
            [5'-pGACTAGTTCTAGTCGAGCGCCGCC(T)15-3']. cDNA was
            cloned in Not I/Sal I sites. EST analysis was performed at
            the NIH Intramural Sequencing Center (NISC)."]

ORIGIN
    Query Match      75.2%; Score 18.8; DB 7; Length 635;
    Best Local Similarity 72.0%; Pred. No. 2.4e+02;
    Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTCTCTACNAACTSGB 25
    |||||:|||||:|||||:|||||:|||||:
Db 402 GTTCGCTTCTTATACCAAGTGSC 426

RESULT 10
AQ990864/c
LOCUS
DEFINITION
    Rf001701 Photorhabdus luminescens strain W14 M13 library
    Photorhabdus luminescens genomic clone PLG01701, genomic survey
    sequence.
ACCESSION
    AQ990864
VERSION
    AQ990864.1 GI:9649458
KEYWORDS
    GSS.
SOURCE
    Photorhabdus luminescens
    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
    Enterobacteriaceae; Photorhabdus.
REFERENCE
    1 (bases 1 to 672)
    ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
    Daborn, P.J., Bowen, D. and Blattner, F.R.
    A genomic sample sequence of the entomopathogenic bacterium
    Photorhabdus luminescens W14: potential implications for virulence
    Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
MEDLINE
10319786
PUBMED
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bserrf@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.

FEATURES
    source
        1. 672
            /organism="Photorhabdus luminescens"
            /mol_type="genomic DNA"
            /strain="W14"
            /db_xref="taxon:29488"
            /clone="PLG01701"
            /dev_stage="primary phase variant"
            /clone_lib="Photorhabdus luminescens strain W14 M13
            library"
            /note="Genomic DNA from strain W14 was size selected (1-2
            kb) and then cloned into M13 Janus."

ORIGIN
    Query Match      75.2%; Score 18.8; DB 8; Length 672;
    Best Local Similarity 72.0%; Pred. No. 2.4e+02;
    Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTCTCTACNAACTSGB 25
    |||||:|||||:|||||:|||||:|||||:
Db 637 GTTCAGCTTCTTATACCAAGTGSC 613

RESULT 11
BI836912
LOCUS
DEFINITION
    603084230F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5223318 5',
    mRNA sequence.
ACCESSION
    BI836912
VERSION
    BI836912.1 GI:15948462
KEYWORDS
    EST.
SOURCE
    Homo sapiens (human)
    ORGANISM
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 706)
    NIH-MGC http://mgi.nci.nih.gov/.
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Life Technologies, Inc.
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LHAM1561 Row: 1 column: 07
    High quality sequence stop: 646.
FEATURES
    source
        1. 706
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clones="IMAGE:5223318"
            /lab_host="DH10B"
            /clone_lib="NIH_MGC_120"
            /note="Organ: pooled pancreas and spleen; Vector:
            pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
            source anonymous pool of spleen and pancreas from 28 yo
            male. Library is oligo-dT primed and directionally cloned
            (EcoRV site is destroyed upon cloning). Average insert
            size 1.5 kb, insert size range 1-2.5 kb. Library is
            normalized and enriched for full-length clones and was
            constructed by C. Gruber (Invitrogen). Research Genetics
            tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN
    Query Match      75.2%; Score 18.8; DB 4; Length 706;
    Best Local Similarity 72.0%; Pred. No. 2.4e+02;
    Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```



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Best Local Similarity 72.0%; Pred: NO. 2.5e+02;
Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTRTACNAACTSGB 25
   |||||:|||||:|||||:
Db 429 GTTCGCTTTCTTATACCAAGTGC 453

Search completed: November 16, 2004, 10:16:31
Job time : 1534 secs

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FEATURES
Source
Location/Qualifiers
1..797
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4610937"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site: 1.
sf11 (ggcgcctcgccc); site 2: sf11 (ggccattatgcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCATTATGCCC-3' and 3' adaptor sequence
5'-ATTCTAGAGGCGAGGCGCGGCACATG-dt(30)EN-3' (where B = A,
C, G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC library."

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ORIGIN

CRJ: NOCC. THIS IS A MIN-ROC LIBRARY:

Query Match 75.2%; Score 18.8; DB 4; Length 797;

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:43 ; Search time 708.5 Seconds  
(without alignments)  
1668.656 Million cell updates/sec

Title: US-10-820-133-4  
Perfect score: 25  
Sequence: 1 agccgcgtttcttctacnaagtsqb 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:★

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1: gb_ba:*
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2: gb_htg:*
3: gb_in:*
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3: gb_1h: *
4: gb_om: *
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5:  gp_ov: *
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6: gb_pat:*
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7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

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10: gb_ro:*
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12: gb_ev:*
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12: gb_ey:*
13: gb_un:*
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13: gb_u1:
14: gb_v1:*
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Pred. No. is the number

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	21.6	86.4	25	6	AR124524	Sequence	
2	21.6	86.4	25	6	AR163175	Sequence	
3	21.6	86.4	25	6	AR493776	Sequence	
4	21.6	86.4	25	6	AX269134	Sequence	
5	21.6	86.4	25	6	AX491643	Sequence	
6	21.6	86.4	25	6	AX498614	Sequence	
7	21.6	86.4	25	6	BD131330	Recombina	
8	21.6	86.4	48	6	AX525436	Sequence	
9	20.4	81.6	25	6	AR124533	Sequence	
10	20.4	81.6	25	6	AR163184	Sequence	
11	20.4	81.6	25	6	AR493785	Sequence	
12	20.4	81.6	25	6	AX269139	Sequence	
13	20.4	81.6	25	6	AX491652	Sequence	
14	20.4	81.6	25	6	AX498623	Sequence	
15	20.4	81.6	25	6	BD131339	Recombina	
16	20.4	81.6	25	6	BD131366	Recombina	
17	20.4	81.6	48	6	BD263257	Compositi	
18	20.4	81.6	48	6	BD263281	Compositi	
19	20.4	81.6	217173	10	AC122188	Mus muscu	

## ALIGNMENTS

RESULT 1		PAT 16-MAY-2001
AR124524	DNA	linear
LOCUS AR124524	25 bp	
DEFINITION Sequence 4 from patent US 6171861.		
ACCESSION AR124524		
VERSION AR124524.1	GI:14109885	
KEYWORDS .		
SOURCE Unknown.		
ORGANISM Unclassified.		
REFERENCE 1 (bases 1 to 25)		
AUTHORS Hartley,J.L. and Brasch,M.A.		
TITLE Recombinational cloning using engineered recombination sites		
JOURNAL Patent: US 6171861-A 4 09-JAN-2001;		
FEATURES Location/Qualifiers		
source 1..25		
/organism="unknown"		
/mol_type="unassigned DNA"		
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Best Local Similarity 100.0%; Pred.No. 2.8;		
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
Oy 1 AGCCWGCCTTCKTRTCNAAAGTSGB 25		
Db 1 AGCCWGCCTTCKTRTCNAAAGTSGB 25		
RESULT 2		PAT 17-OCT-2001
AR163175	DNA	linear
LOCUS AR163175	25 bp	
DEFINITION Sequence 4 from patent US 6270969.		
ACCESSION AR163175		
VERSION AR163175.1	GI:162233683	
KEYWORDS .		
SOURCE Unknown.		
ORGANISM Unclassified.		
REFERENCE 1 (bases 1 to 25)		
AUTHORS Hartley,J.L. and Brasch,M.A.		
TITLE Recombinational cloning using engineered recombination sites		

JOURNAL Patent: US 6270969-A 4 07-AUG-2001;  
 FEATURES Location/Qualifiers  
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 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match 86.4%; Score 21.6; DB 6; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
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QY 1 AGCCGCTTTCTKTRTACNAAGTSG 25  
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 Db 1 AGCCGCTTTCTKTRTACNAAGTSG 25

## RESULT 3

AR493776 AR493776 25 bp mRNA linear PAT 15-MAY-2004  
 LOCUS Sequence 4 from patent US 6720140.  
 DEFINITION  
 ACCESSION AR493776  
 VERSION AR493776.1 GI:472666188  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

## REFERENCE

1 (bases 1 to 25)  
 AUTHORS Hartley, J.L. and Brasch, M.A.  
 TITLE Recombinational cloning using engineered recombination sites  
 JOURNAL Patent: US 6720140-A 4 13-APR-2004;  
 FEATURES Location/Qualifiers  
 source 1..25  
 /organism="unknown"  
 /mol\_type="mRNA"

## ORIGIN

Query Match 86.4%; Score 21.6; DB 6; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTTCTKTRTACNAAGTSG 25  
 |||||  
 Db 1 AGCCGCTTTCTKTRTACNAAGTSG 25

## RESULT 4

AX269134 AX269134 25 bp DNA linear PAT 29-OCT-2001  
 LOCUS Sequence 5 from Patent WO0174861.  
 DEFINITION  
 ACCESSION AX269134  
 VERSION AX269134.1 GI:16542054  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

## REFERENCE

1  
 AUTHORS Ville, R.G., Harrington, K., Murphy, S. and Bateman, A.  
 TITLE Compositions and methods for tissue specific gene regulation  
 JOURNAL therapy  
 Patent: WO 0174861-A 5 11-OCT-2001;  
 MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)  
 FEATURES Location/Qualifiers  
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 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Synthetically generated vector sequence"

## ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTTCTKTRTACNAAGTSG 25  
 |||||  
 Db 1 AGCCGCTTTCTKTRTACNAAGTSG 25

## RESULT 5

AX491643 AX491643 25 bp DNA linear PAT 16-AUG-2002  
 LOCUS Sequence 4 from Patent EP1227147.  
 DEFINITION  
 ACCESSION AX491643  
 VERSION AX491643.1 GI:22324151  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.

## REFERENCE

1  
 AUTHORS Hartley, J.L. and Brasch, M.A.  
 TITLE Recombinational cloning using engineered recombination sites  
 JOURNAL Patent: EP 1227147-A 4 31-JUL-2002;  
 INVITROGEN CORPORATION (US)  
 FEATURES Location/Qualifiers  
 source 1..25  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32644"

## ORIGIN

Query Match 86.4%; Score 21.6; DB 6; Length 25;  
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QY 1 AGCCGCTTTCTKTRTACNAAGTSG 25  
 |||||  
 Db 1 AGCCGCTTTCTKTRTACNAAGTSG 25

## RESULT 6

AX498614 AX498614 25 bp DNA linear PAT 26-SEP-2002  
 LOCUS Sequence 4 from Patent EP1229113.  
 DEFINITION  
 ACCESSION AX498614  
 VERSION AX498614.1 GI:23343411  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.

## REFERENCE

1  
 AUTHORS Hartley, J.L. and Brasch, M.A.  
 TITLE Recombinational cloning using engineered recombination sites  
 JOURNAL Patent: EP 1229113-A 4 07-AUG-2002;  
 INVITROGEN CORPORATION (US)  
 FEATURES Location/Qualifiers  
 source 1..25  
 /organism="unidentified"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32644"

## ORIGIN

Query Match 86.4%; Score 21.6; DB 6; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTTCTKTRTACNAAGTSG 25  
 |||||  
 Db 1 AGCCGCTTTCTKTRTACNAAGTSG 25

## RESULT 7

BD131330 BD131330 25 bp DNA linear PAT 18-SEP-2002  
 LOCUS Recombinational cloning using nucleic acids having recombination  
 DEFINITION sites.  
 ACCESSION BD131330



VERSION BD131330.1 GI:23226275  
 KEYWORDS JP 2002500861-A/4.  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.  
 REFERENCE 1 (bases 1 to 25)  
 AUTHORS Hartley, J.L., Brasch, M.A., Temple, G.P. and Fox, D.K.  
 TITLE Recombinational cloning using nucleic acids having recombination  
 JOURNAL Patent: JP 2002500861-A 4 15-JAN-2002;  
 LIFE TECHNOLOGIES INC  
 COMMENT OS Unknown  
 PN JP 2002500861-A/4  
 PD 15-JAN-2002  
 PF 26-OCT-1998 JP 2000518069  
 PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI  
 JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC  
 C12N15/09, C12Q1/68, C12N15/00  
 CC Description of Unknown Organism: recombination products FH  
 Key Location/Qualifiers  
 FT source 1..25  
 FT /organism="Unknown".  
 FEATURES  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"  
 ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AGCCGCTTTCTCTACNAAGTSG 25  
 Db 1 AGCCGCTTTCTCTACNAAGTSG 25  
 RESULT 8  
 AX525436/c  
 LOCUS AX525436 48 bp DNA linear PAT 21-NOV-2002  
 DEFINITION Sequence 34 from Patent WO02066622.  
 ACCESSION AX525436  
 VERSION AX525436.1 GI:25170322  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.  
 REFERENCE 1  
 AUTHORS Tsutsumi, N., Vind, J. and Patkar, S.A.  
 TITLE Lipolytic enzyme genes  
 JOURNAL Patent: WO 02066622-A 34 29-AUG-2002;  
 Novozymes A/S (DK)  
 FEATURES  
 source Location/Qualifiers  
 1..48  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="051200J24"  
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 Query Match 86.4%; Score 21.6; DB 6; Length 48;  
 Best Local Similarity 76.0%; Pred. No. 2.8;  
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 AGCCGCTTTCTCTACNAAGTSG 25  
 Db 29 AGCCGCTTTCTCTACNAAGTGT 5  
 RESULT 9  
 AR124533  
 LOCUS AR124533 25 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 13 from patent US 6171861.

ACCESSION AR124533  
 VERSION AR124533.1 GI:14109894  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 unclassified.  
 REFERENCE 1 (bases 1 to 25)  
 AUTHORS Hartley, J.L. and Brasch, M.A.  
 TITLE Recombinational cloning using engineered recombination sites  
 JOURNAL Patent: US 6171861-A 13 09-JAN-2001;  
 FEATURES  
 source Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
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 Query Match 81.6%; Score 20.4; DB 6; Length 25;  
 Best Local Similarity 76.0%; Pred. No. 13;  
 Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 AGCCGCTTTCTCTACNAAGTSG 25  
 Db 1 AGCCGCTTTCTCTACNAAGTGG 25  
 RESULT 10  
 AR163184  
 LOCUS AR163184 25 bp DNA linear PAT 17-OCT-2001  
 DEFINITION Sequence 13 from patent US 6270969.  
 ACCESSION AR163184  
 VERSION AR163184.1 GI:16233696  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 unclassified.  
 REFERENCE 1 (bases 1 to 25)  
 AUTHORS Hartley, J.L. and Brasch, M.A.  
 TITLE Recombinational cloning using engineered recombination sites  
 JOURNAL Patent: US 6270969-A 13 07-AUG-2001;  
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 Best Local Similarity 76.0%; Pred. No. 13;  
 Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 AGCCGCTTTCTCTACNAAGTSG 25  
 Db 1 AGCCGCTTTCTCTACNAAGTGG 25  
 RESULT 11  
 AR493785  
 LOCUS AR493785 25 bp mRNA linear PAT 15-MAY-2004  
 DEFINITION Sequence 13 from patent US 6720140.  
 ACCESSION AR493785  
 VERSION AR493785.1 GI:47266206  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 unclassified.  
 REFERENCE 1 (bases 1 to 25)  
 AUTHORS Hartley, J.L. and Brasch, M.A.  
 TITLE Recombinational cloning using engineered recombination sites  
 JOURNAL Patent: US 6720140-A 13 13-APR-2004;  
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 Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTCTCKTRTACNAAGTSG 25  
 Db 1 AGCCTGCTTCTTGTACAAAGTTGG 25

RESULT 12  
 LOCUS AX269139 25 bp DNA linear PAT 29-OCT-2001  
 DEFINITION Sequence 10 from Patent WO01/4861.  
 ACCESSION AX269139  
 VERSION AX269139.1 GI:16542059

KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS Vile, R.G., Harrington, K., Murphy, S. and Bateman, A.  
 TITLE Compositions and methods for tissue specific gene regulation  
 therapy

JOURNAL Patent: WO 01/4861-A 10 11-OCT-2001;  
 MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)

FEATURES  
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 Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTCTCKTRTACNAAGTSG 25  
 Db 1 AGCCTGCTTCTTGTACAAAGTTGG 25

RESULT 13  
 LOCUS AX491652 25 bp DNA linear PAT 16-AUG-2002  
 DEFINITION Sequence 13 from Patent EP1227147.  
 ACCESSION AX491652  
 VERSION AX491652.1 GI:22324160

KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified

REFERENCE 1  
 AUTHORS Hartley, J.L. and Brasch, M.A.

TITLE Recombinational cloning using engineered recombination sites  
 JOURNAL Patent: EP 1227147-A 13 31-JUL-2002;  
 INVITROGEN CORPORATION (US)

FEATURES  
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Qy 1 AGCCGCTTCTCKTRTACNAAGTSG 25  
 Db 1 AGCCTGCTTCTTGTACAAAGTTGG 25

RESULT 14  
 LOCUS AX498623 25 bp DNA linear PAT 26-SEP-2002  
 DEFINITION Sequence 13 from Patent EP1229113.  
 ACCESSION AX498623  
 VERSION AX498623.1 GI:23343420

KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 ORGANISM unclassified.

REFERENCE 1  
 AUTHORS Hartley, J.L. and Brasch, M.A.

TITLE Recombinational cloning using engineered recombination sites  
 JOURNAL Patent: EP 1229113-A 13 07-AUG-2002;  
 INVITROGEN CORPORATION (US)

FEATURES  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32644"

## ORIGIN

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 Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTCTCKTRTACNAAGTSG 25  
 Db 1 AGCCTGCTTCTTGTACAAAGTTGG 25

## RESULT 15

BD131339 25 bp DNA linear PAT 18-SEP-2002  
 LOCUS BD131339  
 DEFINITION Recombinational cloning using nucleic acids having recombination sites.

ACCESSION BD131339  
 VERSION BD131339.1 GI:23226284  
 KEYWORDS JP 2002500861-A/13.  
 SOURCE unidentified  
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 25)  
 AUTHORS Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.

TITLE Recombinational cloning using nucleic acids having recombination sites.  
 JOURNAL Patent: JP 2002500861-A 13 15-JAN-2002;  
 LIFE TECHNOLOGIES INC

COMMENT OS Unknown  
 PN JP 2002500861-A/13  
 PD 15-JAN-2002

PF 26-OCT-1998 JP 2000518069  
 PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI  
 JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DONNA K. FOX PC

C12N15/09, C12Q1/68, C12N15/00  
 CC Description of Unknown Organism: recombination products FH

KEY Key  
 FT source Location/Qualifiers  
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 /organism="Unknown".

FEATURES  
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## ORIGIN

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Qy 1 AGCCGCTTCTCKTRTACNAAGTSG 25  
 Db 1 AGCCTGCTTCTTGTACAAAGTTGG 25

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	21.6	86.4	25	2 AAX78938	Aax78938 Oligonuc
3	21.6	86.4	25	4 AAC87869	Aac87869 Escherich
4	21.6	86.4	25	4 AAF55738	Aaf55738 Recombina
5	21.6	86.4	25	4 AAD14432	Aad14432 Recombina
6	21.6	86.4	25	5 AAS14783	Aas14783 Lambda ph
7	21.6	86.4	25	8 ABT16624	Abt16624 Artificia
8	21.6	86.4	25	9 ACD28279	Acd28279 Nucleic a
9	21.6	86.4	25	9 ACD28479	Acd28479 Nucleic a
10	21.6	86.4	25	10 AAD60561	Aad60561 Core regi
11	21.6	86.4	25	10 ACC44653	Acc44653 Recombina
12	21.6	86.4	25	12 ADL93419	Adl93419 Recombina
13	21.6	86.4	48	6 ABT12773	Abt12773 Thermomyc
14	21.6	86.4	25	2 AAT48222	Aat48222 attL2 cor
15	20.4	81.6	25	2 AAX78947	Aax78947 Oligonuc
16	20.4	81.6	25	2 AAX78974	Aax78974 Oligonuc
17	20.4	81.6	25	4 AAC87878	Aac87878 Escherich
18	20.4	81.6	25	4 AAF55747	Aaf55747 Recombina
19	20.4	81.6	25	4 AAD14441	Aad14441 Recombina
20	20.4	81.6	25	4 AAS14788	Aas14788 Lambda ph
21	20.4	81.6	25	5 AAD14788	Adl4788 Lambda ph

## ALIGNMENTS

## RESULT 1

AAT48213  
ID AAT48213 standard; DNA; 25 BP.

XX AAT48213;

DT 20-OCT-1997 (first entry)

XX M-attL core region.

XX att recombination site; core region; mutation; enhance; recombination;  
KW vector; subcloning; regulation; exchange; ss.

OS Synthetic.

XX WO9640724-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US010082.

XX 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
PT using recombinant proteins and engineered recombination sites in vitro or  
PT in vivo.

XX Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The  
CC core region has at least one engineered mutation that enhances  
CC recombination in vitro in the formation of a co-integrate or Product DNA.  
CC These core regions can be incorporated into novel vector donor DNA  
CC molecules. The nucleic acids, vectors and methods of the invention are  
CC used to obtain chimeric nucleic acid using recombination proteins and  
CC engineered recombination sites in vitro or in vivo. The improved  
CC specificity, speed and yields of the invention facilitates DNA or RNA  
CC subcloning, regulation or exchange useful for any related purpose, e.g.

Abc82125 Core sequ  
Abc16332 Artificia  
Acd28288 Nucleic a  
Acd28488 Nucleic a  
Ada38174 DNA of a  
Aad60570 Core regi  
Acc44662 Recombina  
Adl93428 Recombina  
Aac55543 att site  
Aac55568 Mutationa  
Aac55565 attL site  
Aas06244 PCR prime  
Aas06215 PCR prime  
Aax78942 Oligonuc  
Aac55381 Recombina  
Aas06182 Phase-lam  
Aac87900 Escherich  
Aaf55769 PCR prime  
Aah22543 ATT site  
Aad14460 Recombina  
Acd28430 Engineere  
Acd28609 Engineere  
Ada38196 DNA Oligo  
Adf42420 AttB2 nuc



```

XX 12-APR-2001 (first entry)
XX DT
XX Recombination site m-attL.
XX DE
XX Recombination site; cloning; m-att; ss.
XX KW
XX Unidentified.
XX OS
XX US6171861-B1.
XX PN
XX 09-JAN-2001.
XX PD
XX 12-JAN-1998; 98US-00005476.
XX PF
XX 07-JUN-1995; 95US-00486139.
XX PR
XX 07-JUN-1996; 96US-00663002.
XX PS
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX PA
XX Hartley JL, Brasch MA;
XX PI
XX WPI; 2001-136877/14.
XX DR
XX In vitro cloning of nucleic acid involves mixing vectors comprising
XX PT recombination sites and/or nucleic acid, incubating mixture to produce
XX PT chimeric molecule, contacting hosts with mixture and selecting host.
XX PT
XX Claim 24; Col 46; 73pp; English.
XX PS
XX The present invention relates to a method for in vitro cloning of a
XX CC nucleic acid of interest. The method involves mixing in vitro two vectors
XX CC each comprising at least one recombination site and the nucleic acid of
XX CC interest; incubating the mixture in the presence of at least one
XX CC recombination protein to result in recombination of the recombination
XX CC sites, leading to production of a chimeric nucleic acid molecule
XX CC comprising the nucleic acid of interest; contacting hosts with the
XX CC mixture; and selecting for a host comprising the chimeric nucleic acid
XX CC molecule, and selecting against a host comprising the vectors comprising
XX CC the second vector, to clone the nucleic acid. The present sequence is a
XX CC recombination site, which may be used in the method of the present
XX CC invention
XX CC
XX SQ Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match      86.4%; Score 21.6; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCTKTRTACNAAGTSG 25
   |||||
Db 1 AGCCWGCCTTCTKTRTACNAAGTSG 25

RESULT 5
AADI4432
ID AAD14432 standard; DNA; 25 BP.
XX AC
XX AAD14432;
XX DT
XX 01-NOV-2001 (first entry)
XX DE
XX Recombination site m-attL DNA.
XX KW
XX Recombination site; copy number; replicon; recombinatorial cloning;
XX KW m-attL; db.
XX OS
XX Unidentified.
XX PN
XX US6270969-B1.
XX PD
XX 07-AUG-2001.
XX

XX 20-JAN-1999; 99US-00233492.
XX PF
XX 07-JUN-1995; 95US-00486139.
XX PR
XX 07-JUN-1996; 96US-00663002.
XX XX
XX (INVI-) INVITROGEN CORP.
XX PA
XX Hartley JL, Brasch MA;
XX PI
XX WPI; 2001-488248/53.
XX DR
XX Methods for apposing nucleic acids comprising an expression signal and a
XX PT gene/partial gene, using recombinatorial cloning by incubating the
XX PT nucleic acids in the presence of a recombination protein under conditions
XX PT for recombination.
XX XX
XX Claim 14; Col 18; 76pp; English.
XX PS
XX The invention relates to a method for apposing an expression signal and a
XX CC gene or partial gene, using recombinatorial cloning. The method incubates
XX CC nucleic acids comprising the expression signal and the gene/partial gene
XX CC in the presence of a recombination protein under conditions sufficient to
XX CC cause recombination and therefore appose the expression signal and the
XX CC gene or partial gene. The methods are useful for apposing an expression
XX CC signal and a gene or partial gene using recombinatorial cloning. The
XX CC methods are also useful for changing vectors, constructing genes for
XX CC fusion proteins, changing copy number, changing replicons, cloning into
XX CC phages, and cloning e.g., PCR products (with an attB site at one end and
XX CC a loxP site at the other end), genomic DNAs, and cDNAs. The methods are
XX CC highly specific, rapid, and less labour intensive than prior art methods.
XX CC The present sequence is a recombination site useful for recombination
XX CC cloning
XX CC
XX SQ Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match      86.4%; Score 21.6; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCTKTRTACNAAGTSG 25
   |||||
Db 1 AGCCWGCCTTCTKTRTACNAAGTSG 25

RESULT 6
AAS14783
ID AAS14783 standard; DNA; 25 BP.
XX AC
XX AAS14783;
XX DT
XX 27-FEB-2002 (first entry)
XX DE
XX Lambda phage Int recombinase site core region DNA sequence m-attL.
XX KW
XX Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine;
XX KW syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour;
XX KW recombinase; tumour-specific promoter; hypoxic response element; HRE; ss;
XX KW tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer;
XX KW cytosstatic; gene therapy; Int recombinase site core region; m-attL;
XX KW excisive recombination.
XX XX
XX Bacteriophage lambda.
XX OS
XX WO200174861-A2.
XX PN
XX 11-OCT-2001.
XX PD
XX 30-MAR-2001; 2001WO-US010250.
XX XX
XX 31-MAR-2000; 2000US-0193977P.
XX PR
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX PA
XX

```





XX Claim 14; Page 25; 71pp; English.

PS The invention relates to a vector donor DNA molecule comprising a first

CC DNA segment and a second DNA segment containing at least one selectable

CC marker. The first and second segments are separated either by, in a

CC circular vector donor, a first and a second recombination site, or in a

CC linear vector donor, at least a first recombination site, where each pair

CC of flanking recombination sites are engineered and do not recombine with

CC each other. The nucleic acid molecule, vectors and methods are useful for

CC moving or exchanging segments of DNA molecules using engineered

CC recombination sites and recombination proteins to provide chimeric DNA

CC molecules that have the desired characteristic(s) and/or DNA segment(s).

CC The present sequence represents the nucleic acid core region m-attL

XX Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

SQ

Query Match 86.4%; Score 21.6; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGTTTCKTRTACNAAGTSG 25

Db 1 AGCCGCGTTTCKTRTACNAAGTSG 25

RESULT 9

ID ACD28479 standard; DNA; 25 BP.

XX ACD28479;

AC

XX 09-OCT-2003 (first entry)

DT

XX Nucleic acid core sequence m-attL.

DE

XX Nucleic acid core; m-attL; cointegrate DNA; flanking recombination site;

KW ds.

XX Synthetic.

OS

XX US2003068799-A1.

PN

XX 10-APR-2003.

PD

XX 06-JUN-2002; 2002US-00162879.

PF

XX 07-JUN-1995; 95US-00486139.

PR

XX 07-JUN-1996; 96US-00663002.

PR

XX 20-JAN-1999; 99US-00233493.

PR

XX 02-NOV-1999; 99US-00432085.

XX (INVI-) INVITROGEN CORP.

PA

XX Hartley JL, Brasch MA;

PI

XX WPI; 2003-540884/51.

DR

XX Making Cointegrate DNA molecule, by combining recombination sites

PT flanking the desired DNA segment in insert donor DNA, with the

PT recombination sites of vector donor DNA, using site specific

PT recombination protein.

PS Claim 14; Page 25; 71pp; English.

XX The invention relates to a method of making a cointegrate DNA molecule.

CC The method is useful for making a cointegrate DNA molecule. The method is

CC useful for a variety of DNA exchanges, such as subcloning of DNA, in

CC vitro or in vivo. The method enables efficient and specific recombination

CC of DNA segments using recombination proteins. The method is highly

CC specific, rapid and less labour intensive. The improved specificity,

CC yield and speed of the method facilitates DNA or RNA subcloning,

CC regulation and exchange useful for other related purposes. Since single

CC

CC molecules of the recombinations product can be introduced into a

CC biological host, propagation of the desired product DNA in the absence of

CC other DNA molecules is more readily realised. Reaction conditions can be

CC freely adjusted in vitro to optimise enzyme activities. The present

CC sequence represents the nucleic acid core sequence m-attL

XX Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

SQ

Query Match 86.4%; Score 21.6; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGTTTCKTRTACNAAGTSG 25

Db 1 AGCCGCGTTTCKTRTACNAAGTSG 25

RESULT 10

ADA38165

ID ADA38165 standard; DNA; 25 BP.

XX ADA38165;

AC

XX 20-NOV-2003 (first entry)

DT

XX m-attL DNA sequence indicating generic core region of an attL site.

DE

XX engineered recombination site; cloning; recombinase; subcloning; attB;

KW attP; attL; attR; selectable marker; cointegrate; m-attL; ds.

XX Synthetic.

OS

XX US2003054552-A1.

PN

XX 20-MAR-2003.

PD

XX 30-JAN-2002; 2002US-00058292.

PF

XX 07-JUN-1995; 95US-00486139.

PR

XX 07-JUN-1996; 96US-00663002.

PR

XX 20-JAN-1999; 99US-00233493.

PR

XX 02-NOV-1999; 99US-00432085.

XX (HARTLEY) HARTLEY J L.

PA (BRASCH) BRASCH M A.

PI

XX Hartley JL, Brasch MA;

XX WPI; 2003-585168/55.

DR

XX New Vector Donor DNA molecule, useful for recombinational cloning

PT purposes, comprises a first and a second DNA segment that contains a

PT selectable marker and is separated by a pair of flanking, engineered

PT recombination sites.

PS Claim 14; Page 26; 72pp; English.

XX This invention relates to novel DNA and vectors having engineered

CC recombination sites for use in a cloning method that enables efficient

CC and specific recombination of DNA segments using recombination proteins

CC including recombinases. As such, it provides a method for obtaining

CC chimeric nucleic acids with the desired characteristics, facilitating DNA

CC or RNA subcloning, regulation and/or exchange. The recombination site is

CC derived from attB attP, attL or attR, where the att site is attI, att2 or

CC att3. Engineered mutations of the att sites (either one or multiple

CC mutations) can enhance specificity or efficiency of the recombination

CC reaction and the properties of the product DNA molecules. Accordingly,

CC the present invention describes a nucleic acid molecule comprising at

CC least one DNA segment having at least two engineered recombination sites

CC flanking a selectable marker and/or a desired DNA segment. Furthermore,

CC at least one of the engineered sites must enhance recombination in vitro

CC to form a cointegrate or product DNA molecule. This oligonucleotide

CC sequence is m-attL, a generic DNA sequence indicating the core region of

CC an attL recombination site of the invention.

SQ Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.68; Length 25;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 11

AAAD60561

ID AAD60561 standard; DNA; 25 BP.

XX

AC AAD60561;

XX

DT 18-DEC-2003 (first entry)

XX

DE Core region DNA, m-attL.

XX

KW Recombinational cloning; DNA exchange; core region; ds.

XX

OS Unidentified.

XX

PN US2003100110-A1.

XX

PD 29-MAY-2003.

XX

PF 02-NOV-1999; 99US-00432085.

XX

PR 07-JUN-1995; 95US-00486139.

XX

PR 07-JUN-1996; 96US-00663002.

XX

PR 20-JAN-1999; 99US-00233493.

XX

PA (HARTLEY J L.

XX

PA (BRASCH M A.

XX

PI Hartley JL, Brasch MA;

XX

XX WPI; 2003-730143/69.

XX

PS Claim 14; Page 25; 71pp; English.

XX

CC The invention relates to a vector donor DNA molecule which comprises first and second DNA segments that do not recombine with each other and that contain a selectable marker. The invention also relates to a method for recombinational cloning using engineered recombination sites. The invention is useful for moving or exchanging segments of DNA molecules using engineered recombination sites and recombination proteins to provide chimeric DNA molecules that have the desired characteristic(s) and/or DNA segment(s). The present sequence is a core region DNA. This sequence is used to illustrate the method of the invention

SQ Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 10; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.68; Length 25;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 12

ACC44653

ID ACC44653 standard; DNA; 25 BP.

XX

AC ACC44653;

XX

DT 29-MAY-2003 (first entry)

XX

DE Recombination site related oligonucleotide SEQ ID NO:44.

XX

KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;

XX

KW att site; integrase; recombinase; Aces; gene therapy; transgenic animal;

XX

KW platform artificial chromosome expression system; PCR primer; ss.

XX

OS Synthetic.

XX

PN WO200297059-A2.

XX

PD 05-DEC-2002.

XX

PF 30-MAY-2002; 2002WO-US017452.

XX

PR 30-MAY-2001; 2001US-0294758P.

XX

PR 21-MAR-2002; 2002US-0366891P.

XX

PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX

PI Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;

XX

PI Stewart S, Shellard J;

XX

XX WPI; 2003-140461/13.

XX

PS Claim 43; Page 143; 272pp; English.

XX

CC The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (i) a platform artificial chromosome expression system (Aces) (ii) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an Aces. (ii) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (ii) by cell fusion, lipid-mediated transfection, by a carrier system, microinjection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (ii) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of Aces comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the exemplification of the present invention

SQ Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 10; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 13

ADL93419

ID ADL93419 standard; DNA; 25 BP.

XX



DE	attL2 core region.
XX	
KW	att recombination site; core region; mutation; enhance; recombination;
KW	vector; subcloning; regulation; exchange; ss.
XX	
OS	Synthetic.
XX	
FN	WO9640724-Al.
XX	
PD	19-DEC-1996.
XX	
XX	
PF	07-JUN-1996; 96WO-US010082.
XX	
PR	07-JUN-1995; 95US-00486139.
XX	
PA	(LIFE-) LIFE TECHNOLOGIES INC.
XX	
PI	Hartley JL, Brasch MA;
XX	
DR	WPI; 1997-065168/06.
XX	
XX	
PT	Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT	using recombinant proteins and engineered recombination sites in vitro or
PT	in vivo.
XX	
PS	Claim 14; Page 56; 106pp; English.
XX	
CC	ANT48210-25 are att recombination site core region DNA sequences. The
CC	core region has at least one engineered mutation that enhances
CC	recombination in vitro in the formation of a Cointegrate or Product DNA.
CC	These core regions can be incorporated into novel vector donor DNA
CC	molecules. The nucleic acids, vectors and methods of the invention are
CC	used to obtain chimeric nucleic acid using recombination proteins and
CC	engineered recombination sites in vitro or in vivo. The improved
CC	specificity, speed and yields of the invention facilitates DNA or RNA
CC	subcloning, regulation or exchange useful for any related purpose, e.g.
CC	in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC	or modification of transcribed, replicated, isolated or genomic DNA or
CC	RNA
XX	
SQ	Sequence 25 BP; 5 A; 5 C; 6 G; 9 T; 0 U; 0 Other;
	Query Match 81.6%; Score 20.4; DB 2; Length 25;
	Best Local Similarity 76.0%; Pred. No. 2.7;
	Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy	1 AGCCGCGCTTCTKTRTACNAAGTSGB 25      :     :
Db	1 AGCCTGCTTCTTGTAACAAAGTTGG 25      :     :

Search completed: November 16, 2004, 04:02:47  
Job time : 168.8 secs



Query Match 86.4%; Score 21.6; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTCKTRTACNAAGTSG 25  
|||||  
Db 1 AGCCWGCCTTCKTRTACNAAGTSG 25  
|||||

## RESULT 2

US-09-005-476-4  
; Sequence 4, Application US/09005476  
; Patent No. 6171861  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/005,476  
; FILING DATE: herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2500  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA

US-09-005-476-4

Query Match 86.4%; Score 21.6; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTCKTRTACNAAGTSG 25  
|||||  
Db 1 AGCCWGCCTTCKTRTACNAAGTSG 25  
|||||

## RESULT 3

US-09-233-492-4  
; Sequence 4, Application US/09233492  
; Patent No. 6270969  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington

STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/233,492  
FILING DATE: 20-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA

US-09-233-492-4

Query Match 86.4%; Score 21.6; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTCKTRTACNAAGTSG 25  
|||||  
Db 1 AGCCWGCCTTCKTRTACNAAGTSG 25  
|||||

## RESULT 4

US-09-296-280-4  
; Sequence 4, Application US/09296280  
; Patent No. 6277608  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850007  
; CURRENT APPLICATION NUMBER: US/09/296,280  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: US 09/177,387  
; EARLIER FILING DATE: 1998-10-23  
; EARLIER APPLICATION NUMBER: US 60/065,930  
; EARLIER FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-296-280-4

Query Match 86.4%; Score 21.6; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 5  
US-09-498-074-4  
; Sequence 4, Application US/09498074  
; Patent No. 6534264  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brach, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/498,074  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
; US-09-498-074-4

Query Match 86.4%; Score 21.6; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 6  
US-09-498-074-4  
; Sequence 4, Application US/09498074  
; Patent No. 6720140  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brach, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/498,074  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
; US-09-498-074-4

Query Match 86.4%; Score 21.6; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 7  
PCT-US96-10082A-4  
; Sequence 4, Application PC/TUS9610082A  
; GENERAL INFORMATION:  
; APPLICANT: Life Technologies, Inc.  
; APPLICANT: 8717 Grovemont Circle  
; APPLICANT: Gaithersburg, MD 20884-9980  
; APPLICANT: United States of America  
; APPLICANT: Brach, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 86.4%; Score 21.6; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 8  
US-09-498-074-4  
; Sequence 4, Application US/09498074  
; Patent No. 6720140  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brach, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICANT: Hartley, James L.  
APPLICANT: Brach, Michael A.  
TITLE OF INVENTION: Recombinational Cloning Using Engineered  
TITLE OF INVENTION: Recombination Sites  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 New York Ave., N. W. Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,074  
FILING DATE: 04-Feb-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,476  
FILING DATE: 12-JAN-1998  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-498-074-4

Query Match 86.4%; Score 21.6; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 9  
PCT-US96-10082A-4  
; Sequence 4, Application PC/TUS9610082A  
; GENERAL INFORMATION:  
; APPLICANT: Life Technologies, Inc.  
; APPLICANT: 8717 Grovemont Circle  
; APPLICANT: Gaithersburg, MD 20884-9980  
; APPLICANT: United States of America  
; APPLICANT: Brach, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/498,074  
; FILING DATE: 04-Feb-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-498-074-4

Query Match 86.4%; Score 21.6; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 10  
PCT-US96-10082A-4  
; Sequence 4, Application PC/TUS9610082A  
; GENERAL INFORMATION:  
; APPLICANT: Life Technologies, Inc.  
; APPLICANT: 8717 Grovemont Circle  
; APPLICANT: Gaithersburg, MD 20884-9980  
; APPLICANT: United States of America  
; APPLICANT: Brach, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 86.4%; Score 21.6; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 11  
PCT-US96-10082A-4  
; Sequence 4, Application PC/TUS9610082A  
; GENERAL INFORMATION:  
; APPLICANT: Life Technologies, Inc.  
; APPLICANT: 8717 Grovemont Circle  
; APPLICANT: Gaithersburg, MD 20884-9980  
; APPLICANT: United States of America  
; APPLICANT: Brach, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 86.4%; Score 21.6; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 12  
US-09-498-074-4  
; Sequence 4, Application US/09498074  
; Patent No. 6720140  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brach, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-4

Query Match 86.4%; Score 21.6; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCGCTTTCKTRTACNAAGTSGB 25
   |||||
Db 1 AGCCGCGCTTTCKTRTACNAAGTSGB 25
   |||||

RESULT 8
US-09-233-493-13
; Sequence 13, Application US/09233493
; Patent No. 614357
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCGCGCTTTCKTRTACNAAGTSGB 25
   |||||
Db 1 AGCCGCGCTTTCTGTACAAAGTTGG 25
   |||||

RESULT 9
US-09-005-476-13
; Sequence 13, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-13

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCGCGCTTTCKTRTACNAAGTSGB 25
   |||||
Db 1 AGCCGCGCTTTCTGTACAAAGTTGG 25
   |||||

RESULT 10
US-09-233-492-13
; Sequence 13, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
```



ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
STREET: 1100 New York Ave., N. W. Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/233,492  
FILING DATE: 20-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cdna  
US-09-233-492-13

Query Match 81.6%; Score 20.4; DB 3; Length 25;  
Best Local Similarity 76.0%; Pred. No. 0.23; Indels 0; Gaps 0;  
Matches 19; Conservative 4; Mismatches 2;

Qy 1 AGCCGCTTTCTKTRTACNAAGTSG 25  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 1 AGCCTGCTTTCTTGACAAAGTTGG 25

## RESULT 11

US-09-296-280-13  
; Sequence 13, Application US/09296280  
; Patent No. 6277608  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850007  
; CURRENT APPLICATION NUMBER: US/09/296,280  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: US 09/177,387  
; EARLIER FILING DATE: 1998-10-23  
; EARLIER APPLICATION NUMBER: US 60/065,930  
; EARLIER FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
US-09-296-280-13

Query Match 81.6%; Score 20.4; DB 3; Length 25;  
Best Local Similarity 76.0%; Pred. No. 0.23; Indels 0; Gaps 0;  
Matches 19; Conservative 4; Mismatches 2;

Qy 1 AGCCGCTTTCTKTRTACNAAGTSG 25  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 1 AGCCTGCTTTCTTGACAAAGTTGG 25

## RESULT 12

US-09-296-280-40  
; Sequence 40, Application US/09296280  
; Patent No. 6277608  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850007  
; CURRENT APPLICATION NUMBER: US/09/296,280  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: US 09/177,387  
; EARLIER FILING DATE: 1998-10-23  
; EARLIER APPLICATION NUMBER: US 60/065,930  
; EARLIER FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 40  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
US-09-296-280-40

Query Match 81.6%; Score 20.4; DB 3; Length 25;  
Best Local Similarity 72.0%; Pred. No. 0.23; Indels 0; Gaps 0;  
Matches 18; Conservative 6; Mismatches 1;

Qy 1 AGCCGCTTTCTKTRTACNAAGTSG 25  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 1 ASCCGCTTTTTRTACWAASTKGW 25

## RESULT 13

US-09-498-074-13  
; Sequence 13, Application US/09498074  
; Patent No. 6534264  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/498,074  
; FILING DATE: (Herewith)  
; CLASSIFICATION:

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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ US-09-498-074-13

Query Match      81.6%; Score 20.4; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCGCTTTCTKTRTACNAAGTSGB 25
Db 1 AGCCGCTTTCTTGACAAAGTTGG 25

RESULT 14
US-09-498-074-13
/ Sequence 13, Application US/09498074
/ Patent No. 6720140
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ Recombination Sites
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/498,074
/ FILING DATE: 04-Feb-2000
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
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/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-498-074-13

Query Match      81.6%; Score 20.4; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Db 1 AGCCGCTTTCTTGACAAAGTTGG 25

RESULT 15
PCT-US96-10082A-13
/ Sequence 13, Application PC/TUS9610082A
/ GENERAL INFORMATION:
/ APPLICANT: Life Technologies, Inc.
/ APPLICANT: 8717 Grovemont Circle
/ APPLICANT: Gaithersburg, MD 20884-9980
/ APPLICANT: United States of America
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ Recombination Sites
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/10082A
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ PCT-US96-10082A-13

Query Match      81.6%; Score 20.4; DB 5; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCGCTTTCTKTRTACNAAGTSGB 25
Db 1 AGCCGCTTTCTTGACAAAGTTGG 25

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Job time : 35.9 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 ; Search time 314 Seconds  
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430.015 Million cell updates/sec

Title: US-10-820-133-4

Perfect score: 25

Sequence: 1 agcwgcttcttctacnaagtagb 25

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21.6	86.4	25	9	US-09-822-634-5
3	21.6	86.4	25	9	US-09-907-900-4
4	21.6	86.4	25	9	US-09-907-719-4
5	21.6	86.4	25	10	US-09-432-085-4
6	21.6	86.4	25	10	US-09-985-448-4
7	21.6	86.4	25	14	US-10-058-292-4
8	21.6	86.4	25	14	US-10-058-291-4
9	21.6	86.4	25	14	US-10-162-879-4
10	21.6	86.4	25	15	US-10-161-403-4
11	21.6	86.4	25	15	US-10-300-892-4
12	21.6	86.4	25	16	US-10-680-316-4

13	21.6	86.4	25	17	US-10-815-730-4
14	21.6	86.4	25	17	US-10-820-133-4
15	21.6	86.4	25	18	US-10-161-408-36
16	21.6	86.4	25	18	US-10-796-868A-4
17	21.6	86.4	48	17	US-10-250-824-34
18	20.4	81.6	25	9	US-09-855-797A-13
19	20.4	81.6	25	9	US-09-855-797A-40
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34	20.4	81.6	25	15	US-10-300-892-40
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36	20.4	81.6	25	16	US-10-680-316-40
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41	20.4	81.6	25	18	US-10-161-408-44
42	20.4	81.6	25	18	US-10-796-868A-13
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45	20	80.0	25	9	US-09-732-914-9

ALIGNMENTS

RESULT 1

US-09-855-797A-4

; Sequence 4, Application US/09855797A

; Patent No. US20020094574A1

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.

; APPLICANT: Fox, Donna K.

; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

; TITLE OF INVENTION: Recombination Sites

; FILE REFERENCE: 0942.2850008

; CURRENT APPLICATION NUMBER: US/09/855,797A

; CURRENT FILING DATE: 2001-05-16

; PRIOR FILING DATE: 1999-04-22

; PRIOR FILING DATE: 1997-10-24

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; NAME/KEY: OTHER

; LOCATION: 18

; OTHER INFORMATION: "n" may be any nucleotide

; OTHER INFORMATION: Description of Unknown Organism: recombination

; OTHER INFORMATION: products

US-09-855-797A-4

Query Match 86.4%; Score 21.6; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.4;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25  
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Db 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25

RESULT 2  
US-09-822-634-5  
; Sequence 5, Application US/09822634  
; Patent No. US20020150556A1  
; GENERAL INFORMATION:  
; APPLICANT: Vile, Richard G.  
; APPLICANT: Harrington, Kevin  
; APPLICANT: Bateman, Andrew  
; APPLICANT: Murphy, Steven  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE  
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY  
; FILE REFERENCE: 07039-289001  
; CURRENT APPLICATION NUMBER: US/09/822,634  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/193,977  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated vector sequence  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(25)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-822-634-5

Query Match 86.4%; Score 21.6; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
US-09-907-900-4  
; Sequence 4, Application US/09907900  
; Patent No. US20020172997A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.285004  
; CURRENT APPLICATION NUMBER: US/09/907,900  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-900-4

Query Match 86.4%; Score 21.6; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25

RESULT 4  
US-09-907-719-4  
; Sequence 4, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.285004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-719-4

Query Match 86.4%; Score 21.6; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25

RESULT 5  
US-09-432-085-4  
; Sequence 4, Application US/09432085  
; Publication No. US20030100110A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,085

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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Db 1 AGCCWGCCTTCKTRTACNAAGTSGB 25
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RESULT 7
US-10-058-292-4
; Sequence 4, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/058,292
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
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US-10-058-292-4
Query Match 86.4%; Score 21.6; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 8
US-10-058-291-4
; Sequence 4, Application US/10058291
; Publication No. US2003006451A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brasch, Michael A.

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; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
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; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/10/058,291
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; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-058-291-4

Query Match 86.4%; Score 21.6; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25

RESULT 9
US-10-162-879-4
; Sequence 4, Application US/10162879
; Publication No. US2003006879A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
;
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-162-879-4

Query Match 86.4%; Score 21.6; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25
Db 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25

RESULT 10
US-10-161-403-44
; Sequence 44, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: m-attL
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: 18
; OTHER INFORMATION: n is a o r g o r c o r t/u
US-10-161-403-44

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Query Match      86.4%; Score 21.6; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGCCWGCCTTCTCKTRTACNAAGTSG 25
    |||||
Db 1 AGCCWGCCTTCTCKTRTACNAAGTSG 25
    |||||

RESULT 11
US-10-300-892-4
; Sequence 4, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-4

Query Match      86.4%; Score 21.6; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGCCWGCCTTCTCKTRTACNAAGTSG 25
    |||||
Db 1 AGCCWGCCTTCTCKTRTACNAAGTSG 25
    |||||

RESULT 12
US-10-680-316-4
; Sequence 4, Application US/10680316
; Publication No. US20040063207A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/680,316
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-680-316-4

Query Match      86.4%; Score 21.6; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGCCWGCCTTCTCKTRTACNAAGTSG 25
    |||||
Db 1 AGCCWGCCTTCTCKTRTACNAAGTSG 25
    |||||

RESULT 13
US-10-815-730-4
; Sequence 4, Application US/10815730
; Publication No. US20040171156A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/815,730
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-815-730-4

Query Match      86.4%; Score 21.6; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGCCWGCCTTCTCKTRTACNAAGTSG 25
    |||||
Db 1 AGCCWGCCTTCTCKTRTACNAAGTSG 25
    |||||

RESULT 14
US-10-820-133-4
; Sequence 4, Application US/10820133
; Publication No. US20040171157A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/820,133
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
```

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/ FILE REFERENCE: 0942.2850004
/ CURRENT APPLICATION NUMBER: US/10/820,133
/ CURRENT FILING DATE: 2004-04-08
/ PRIOR APPLICATION NUMBER: US/09/177,387A
/ PRIOR FILING DATE: 1998-10-23
/ PRIOR APPLICATION NUMBER: US 60/065,930
/ PRIOR FILING DATE: 1997-10-24
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ NAME/KEY: OTHER
/ LOCATION: 18
/ OTHER INFORMATION: "n" may be any nucleotide
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: recombination
/ OTHER INFORMATION: products
US-10-820-133-4

Query Match      86.4%; Score 21.6; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTCKTRTACNAAGTSG 25
   |||||
Db 1 AGCCWGCCTTCKTRTACNAAGTSG 25

RESULT 15
US-10-161-408-36
/ Sequence 36, Application US/10161408
/ Publication No. US20040214290A1
/ GENERAL INFORMATION:
/ APPLICANT: Perez, Carl
/ APPLICANT: Fabijanski, Steven
/ APPLICANT: Perkins, Edward
/ TITLE OF INVENTION: Plant Artificial Chromosomes, Uses thereof, and Methods of Preparation
/ FILE REFERENCE: 24601-419
/ CURRENT APPLICATION NUMBER: US/10/161,408
/ CURRENT FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: US 60/294,687
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: US 60/296,329
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 36
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: m-attL recognition sequence
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: 18
/ OTHER INFORMATION: n is a or g or c or t/u
US-10-161-408-36

Query Match      86.4%; Score 21.6; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTCKTRTACNAAGTSG 25
   |||||
Db 1 AGCCWGCCTTCKTRTACNAAGTSG 25

Search completed: November 16, 2004, 11:14:59
Job time : 315.1 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds  
(without alignments)  
594.643 Million cell updates/sec

Title: US-10-820-133-4

Perfect score: 25  
Sequence: 1 agccwgttcttcttaacnaagtsb 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsl1:\*  
9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.6	86.4	1076	7	CK217224
2	21.6	86.4	1192	7	CK210997
C 3	20.4	81.6	564	8	BH110378
C 4	20.4	81.6	579	8	BH110594
5	20	80.0	69	7	CF652201
6	20	80.0	79	7	CF651937
C 7	20	80.0	80	6	CB394681
8	20	80.0	84	6	CB400948
9	20	80.0	87	7	CF652842
10	20	80.0	89	7	CF651862
11	20	80.0	89	7	CF652759
12	20	80.0	89	7	CF653076
13	20	80.0	93	7	CF652843
14	20	80.0	95	7	CF651695
15	20	80.0	95	7	CF651816
16	20	80.0	95	7	CF651859
17	20	80.0	95	7	CF651861
18	20	80.0	95	7	CF651893
19	20	80.0	95	7	CF651957
20	20	80.0	95	7	CF651975
21	20	80.0	95	7	CF652127
22	20	80.0	95	7	CF652128
23	20	80.0	95	7	CF652167
24	20	80.0	95	7	CF652261

25	20	80.0	95	7	CF652333	49-L02013
26	20	80.0	95	7	CF652453	56-L02052
27	20	80.0	95	7	CF652502	59-L02052
28	20	80.0	95	7	CF652546	62-L02036
29	20	80.0	95	7	CF652555	62-L02057
30	20	80.0	95	7	CF652580	64-L02036
31	20	80.0	95	7	CF652581	64-L02036
32	20	80.0	95	7	CF652614	66-L02036
33	20	80.0	95	7	CF652617	66-L02052
34	20	80.0	95	7	CF652673	69-L02058
35	20	80.0	95	7	CF652698	71-L02036
36	20	80.0	95	7	CF652700	71-L02052
37	20	80.0	95	7	CF652763	75-L02035
38	20	80.0	95	7	CF652837	79-L02057
39	20	80.0	95	7	CF652855	80-L02058
40	20	80.0	95	7	CF652890	83-L02013
41	20	80.0	95	7	CF652914	84-L02036
42	20	80.0	95	7	CF652955	86-L02057
43	20	80.0	95	7	CF652980	88-L02052
44	20	80.0	95	7	CF653038	92-L02013
45	20	80.0	95	7	CF653059	93-L02035

#### ALIGNMENTS

RESULT 1  
CK217224  
LOCUS  
DEFINITION FGAS029225 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum  
aestivum CDNA, mRNA sequence.  
CK217224  
CK217224.1 GI:396233328  
EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 1076)  
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,  
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,  
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,  
Penniket, C., Roach, J.L. and Sarhan, F.  
Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
Unpublished (2003)  
Contact: Wm L Crosby  
Bioinformatics  
University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033  
Email: fgas\_est@cs.usask.ca  
This sequence is the direct result of the Base calling software  
Phred (default parameters). It is the raw base calls. To aid in the  
identification of the high quality insert the software Lucy  
(default parameters) has been run on this sequence. Lucy identified  
the region [17..730].  
Plate: LG8025 row: A column: 06.  
Location/Qualifiers  
1..1076  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone\_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"  
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown  
(50%) and leaf (50%) tissues from wheat cultivar Norstar  
after short exposure times to low temperature in the light  
and in the dark. 12 mRNA populations were combined before  
constructing the library. The first 6 populations: After 7  
days of growth at 20C from wheat cultivar Norstar after  
short exposure times to low temperature in the light and

in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4C in the light. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20C, wheat plants were transferred to 4C in the dark. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACGTGCAGCAGGACACTGACATGCTGCAGGATGAGAA). "

CGACGGGACGAGGAGGACATGACATGGATGAGGAGTAGAAA). "

ORIGIN

Query Match 86.4%; Score 21.6; DB 7; Length 1076;  
Best Local Similarity 76.0%; Pred. No. 8.2;  
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCTKTRTACNAAGTSG 25  
|||||:|||||:|||||:|||||:  
Db 760 AGCCAGCTTTCTTGTACAAAGTGGC 784

RESULT 2				
CK210997				
LOCUS	CK210997	1192 bp	linear	EST 08-DEC-2003
DEFINITION	FGAS022824	Triticum aestivum	FGAS: Library 5 GATE 7	Triticum aestivum cDNA, mRNA sequence.

CK210997  
ACCESSION  
CK210997.1  
VERSION  
EST.  
KEYWORDS  
GI:39573387

SOURCE	ORGANISM
Triticum aestivum (bread wheat)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Triticum aestivum	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
	Pooidae; Triticeae; Triticum.

REFERENCE  
1 (bases 1 to 1192)  
AUTHORS  
Allard, F., Crosby, W. L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Grat, R., Gulick, P., Hrycan, L. D., Laroche, A., Links, M. G., McCarthy, E. L., Monroy, A., Muzak, I., Nilson, D., Pennick, C., Roach, J. L. and Sarhan, F.

**TITLE** Functional Genomics of Abiotic Stress In Wheat and Canola Crops  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Wm L Crosby

**Bioinformatics**  
University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033

Fax: 506 566 2553  
 Email: f9as\_estcs@cs.usask.ca  
 This sequence is the direct result of the Base calling software  
 Phred (default parameters). It is the raw base calls. To aid in the  
 identification of the high quality insert the software Lucy  
 (default parameters) has been run on this sequence. Lucy identified  
 the region [125,552].  
 Plate: L5B024 row: L column: 01.

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FEATURES
source
1. .1192
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="ta:09.4565"

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/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"
/note="Vector: pCMV.SPORT6; Crown and developmental stages
of spike formation in wheat cultivar Norstar. 4 mRNA

```

populations were combined before constructing the library. The first mRNA population is from 1cm crown sections after 30 days of cold acclimation. The second is from 1cm crown sections after 11 days of deacclimation (before deacclimation plants were fully vernalized for 49 days). The third is from different developmental stages of spike formation (5 to 50mm) that still have not emerged from the leaf (dissection required). The last is from different developmental stages of spike and seed formation after having emerged from the leaf (visible). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with Not I."

## ORIGIN

Query Match	86.4%;	Score 21.6;	DB 7;	Length 1192;
Best Local Similarity	76.0%;	Pred. No. 8.4;		

QY 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25  
|||||:|||||:|||||:|||||:|:  
Db 650 AGCCAGCTTTCTTGTTACAAAGTGTT 674

RESULT 3  
BH110378/c

LOCUS	BH110378	564 bp	DNA	linear	GSS 19-JUL-2001
DEFINITION	RPCI-24-367J19.TJ RPCI-24 Mus musculus genomic clone RPCI-24-367J19, genomic survey sequence. RPCI-24-367J19, genomic survey sequence.				

ACCESSION BH110378  
VERSION BH110378.1 GI:14944438  
KEYWORDS GSS.

**SOURCE** *Mus musculus* (house mouse)

ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 564)

## REFERENCES

**TITLE** Mouse BAC End Sequences from Library RPCR-24  
**JOURNAL** Unpublished (1999)

COMMENT

Other\_GSSS: KPCI-24-367019.1V  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208

Email: [sznao@tigr.org](mailto:sznao@tigr.org)  
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderingframe.htm>). BAC end page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
Plate: 367 row: J column: 19

```

seq primer: 5'p
Class: BAC ends.
Location/Qualifiers
    1..564
source
FEATURES

```

307

```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-367J19"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTRABAC1; Site 1: BamH1; Site 2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTRABAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."

```

```

ORIGIN
Query Match      81.6%; Score 20.4; DB 8; Length 564;
Best Local Similarity 76.0%; Pred. No. 30;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTCTCTACNAAGTSGB 25
|||||:|||||:|||||:|||||:
Db 517 AGCCGCTTCTCTATACAAAGTAGG 493

RESULT 4
BH110594/c
LOCUS
DEFINITION
  RPCI-24-367L19.TJ RPCI-24 Mus musculus genomic clone
  RPCI-24-367L19, genomic survey sequence.
ACCESSION
  BH110594
VERSION
  BH110594.1 GI:14944870
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 579)
AUTHORS
  Zhao,S., Niemman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
  Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregorgis,B.,
  Russell,D., de Jong,P. and Fraser,C.M.
  Mouse BAC End Sequences from Library RPCI-24
  Unpublished (1999)
TITLE
  Other GSSs: RPCI-24-367L19.TV
JOURNAL
  Contact: Shaying Zhao
COMMENT
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: szhao@tigr.org
  Clones are derived from the mouse BAC library RPCI-24. For BAC
  library availability, please contact Pieter de Jong
  (pdejong@mail.cho.org). Clones may be purchased from BACPAC
  Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
  page: http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html
  Plate: 367 row: L column: 19
  Seq primer: SP6
  Class: BAC ends.
FEATURES
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  Location/Qualifiers
  1..579
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="RPCI-24-367L19"
    /sex="Male"
    /cell_type="Spleen/Brain"
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  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
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AUTHORS
  Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
  Mitchell-Olds,T. and Weishaar,B.
  Large-scale identification and analysis of genome-wide
  single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
  Genome Res. 13 (6), 1250-1257 (2003)
JOURNAL
  22683290
MEDLINE
  12799357
PUBMED
  Contact: Weishaar B
COMMENT
  ADIS DNA core facility at MP12
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@mpiz-koeln.mpg.de
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    and development of methods for genome-wide mutation
    detection' PI: Bernd Weishaar Sequence submission managed
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    for further information."
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1 (bases 1 to 79)
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weishaar,B.
Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
22683290
12799357
PUBMED
COMMENT
Contact: Weissshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
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was made at the Max-Planck-Institute for Plant Breeding
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'Establishment of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection' PI: Bernd Weissshaar Sequence submission managed
by RZPD/GABI-Primary database: http://gabi.rzpd.de This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."
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OSTR142B12_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB394681
VERSION
CB394681.1 GI:30736392
KEYWORDS
EST.
ORGANISM
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 80)
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1 (bases 1 to 80)
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weishaar,B.
Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
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PUBMED
COMMENT
Contact: Weissshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
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was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites SalI-NotI,
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compatible; Note: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity,
'Establishment of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection' PI: Bernd Weissshaar Sequence submission managed
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for further information."
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DEFINITION
OSTR142B12_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
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KEYWORDS
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 80)
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Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weishaar,B.
Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
22683290
12799357
PUBMED
COMMENT
Contact: Weissshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
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VERSION
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Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
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Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
Tolias,P., Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet. (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
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Db 55 ACCCAGCTTCTTGTCACAAAGTGCT 31
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
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Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
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Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
Tolias,P., Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet. (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute

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Wassilewskija-0; roots from three weeks old plants grown on MS-plates at 26M-OC with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sall-NotI, primer sites and orientation:  
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 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

## ORIGIN

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ACCESSION CF652759  
 VERSION CF652759.1 GI:37429556  
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 SOURCE Arabidopsis thaliana (thale cress)

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 89)

## REFERENCE

Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.  
 Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana  
 Genome Res. 13 (6), 1250-1257 (2003)  
 22683220  
 12799357

## COMMENT

Contact: Weisshaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: [weisshaar@mpiz-koeln.mpg.de](mailto:weisshaar@mpiz-koeln.mpg.de)  
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 primer sites and orientation:

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ACCESSION CF653076  
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 KEYWORDS EST.

## SOURCE

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 Arabidopsis thaliana

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 89)

## REFERENCE

Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.  
 Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana  
 Genome Res. 13 (6), 1250-1257 (2003)  
 22683290  
 12799357

## COMMENT

Contact: Weisshaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: [weisshaar@mpiz-koeln.mpg.de](mailto:weisshaar@mpiz-koeln.mpg.de)  
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## ORIGIN

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CF652843

VERSION CF652843.1 GI:37429720

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

## ORGANISM

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 93)

Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.

Large-scale identification and analysis of genome-wide

single-nucleotide polymorphisms for mapping in Arabidopsis thaliana  
Genome Res. 13 (6), 1250-1257 (2003)

22683290

PUBMED 12799357

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

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was made at the Max-Planck-Institute for Plant Breeding  
Research, Cologne, Germany; cloning sites Sali-NotI,  
primer sites and orientation:

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GABI Arabidopsis Verbund I: Genetic Diversity,  
'Establishment of high-efficiency SNP-based mapping tools  
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by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This  
clone is available from RZPD; contact RZPD (clone@rzpd.de)  
for further information."

## ORIGIN

Query Match

Best Local Similarity

Matches 18; Conservative

80.0%; Score 20; DB 7; Length 95;

72.0%; Pred. No. 33;

Mismatches 2; Indels 0; Gaps 0;

Query Match

Best Local Similarity

Matches 18; Conservative

80.0%; Score 20; DB 7; Length 93;

72.0%; Pred. No. 33;

Mismatches 2; Indels 0; Gaps 0;

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1 AGCCGCTTTCTKTRTACNAAGTSG 25

Db 50 ACCGAGCTTTCTGTACAAAGTGT 74

## RESULT 14

CF651695

## LOCUS

DEFINITION 07-L020525-066-003-N01-SP6P MP1Z-ADIS-066 Arabidopsis thaliana CDNA

CF651695

VERSION CF651695.1 GI:37427478

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 95)

Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.

Large-scale identification and analysis of genome-wide

single-nucleotide polymorphisms for mapping in Arabidopsis thaliana  
Genome Res. 13 (6), 1250-1257 (2003)

22683290

PUBMED 12799357

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

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Seq primer: SP6P;

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Wasilewskija-0; roots from three weeks old plants grown  
on MS-plates at 26M-OC with 16 hours light/day; library  
was made at the Max-Planck-Institute for Plant Breeding  
Research, Cologne, Germany; cloning sites Sali-NotI,  
primer sites and orientation:

SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY  
compatible; Note: Sequencing granted in the context of the  
GABI Arabidopsis Verbund I: Genetic Diversity,  
'Establishment of high-efficiency SNP-based mapping tools  
and development of methods for genome-wide mutation  
detection' PI: Bernd Weisshaar Sequence submission managed  
by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This  
clone is available from RZPD; contact RZPD (clone@rzpd.de)  
for further information."





RESULT 2					
AR163176	AR163176	Sequence 5 from patent US 6270969.	25 bp	DNA	linear
LOCUS					
DEFINITION	AR163176				
ACCESSION	AR163176				
VERSION	AR163176.1	GI:16233684			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 25)				
TITLE	Hartley,J.L. and Brasch,M.A.				
	Recombinational cloning using engineered recombination sites				

JOURNAL Patent: US 6270969-A 5 07-AUG-2001;  
FEATURES Location/Qualifiers  
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Db 1 GTTCAGCTTTTKTRTACNAAGTSGB 25

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AR493777  
LOCUS 25 bp mRNA linear PAT 15-MAY-2004  
DEFINITION Sequence 5 from patent US 6720140.  
ACCESSION AR493777  
VERSION AR493777.1 GI:472666190  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 25)  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: US 6720140-A 5 13-APR-2004;  
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Db 1 GTTCAGCTTTTKTRTACNAAGTSGB 25

RESULT 4  
AX491644  
LOCUS 25 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 5 from Patent EP1227147.  
ACCESSION AX491644  
VERSION AX491644.1 GI:22324152  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: EP 1227147-A 5 31-JUL-2002;  
INVTROGEN CORPORATION (US)  
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JOURNAL Patent: US 6270969-A 5 07-AUG-2001;  
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QY 1 GTTCAGCTTTTKTRTACNAAGTSGB 25  
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Db 1 GTTCAGCTTTTKTRTACNAAGTSGB 25

RESULT 5  
AX498615  
LOCUS 25 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 5 from Patent EP1229113.  
ACCESSION AX498615  
VERSION AX498615.1 GI:23343412  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: EP 1229113-A 5 07-AUG-2002;  
INVTROGEN CORPORATION (US)  
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Db 1 GTTCAGCTTTTKTRTACNAAGTSGB 25

RESULT 6  
AX787513  
LOCUS 25 bp DNA linear PAT 17-JUL-2003  
DEFINITION Sequence 30 from Patent WO03044207.  
ACCESSION AX787513  
VERSION AX787513.1 GI:32954587  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Nomura,N., Goshima,N., Kisu,Y. and Sono,S.  
TITLE Method for the preparation of nucleic acids  
JOURNAL Patent: WO 03044207-A 30 30-MAY-2003;  
Invitrogen Japan K.K. (JP) ; National Institute of Advanced  
Industrial Science and Technology (JP)  
FEATURES Location/Qualifiers  
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Best Local Similarity 76.0%; Pred. No. 7.6;  
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTKTRTACNAAGTSGB 25  
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Db 1 GTTCAGCTTTCTTGTCACAAAGTGT 25

RESULT 7  
BD131331  
LOCUS 25 bp DNA linear PAT 18-SEP-2002  
DEFINITION Recombinational cloning using nucleic acids having recombination  
sites.  
ACCESSION BD131331

Matches	19; Conservative	5; Mismatches	1; Indels	0; Gaps	0
Qy	1	GTTCAGCTTTTKTRTACNAAGTSGB 25			
Db	1	GTTCAGCTTTCTTGTTACAAAGTGGT 25			
RESULT 9					
LOCUS	CQ758822	37 bp	DNA	linear	PAT 01-MAR-2004
DEFINITION	Sequence 13 from Patent WO2003106691.				
ACCESSION	CQ758822				
VERSION	CQ758822.1	GI:44848843			
KEYWORDS	.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
	artificial sequences.				
REFERENCE	1				
AUTHORS	Boesten,W.H., Raenakers-Franken,P.C., Sonke,T., Euverink,G.J. and Grijpstra,P.				
TITLE	POLYPEPTIDES HAVING H-AMINO ACID AMIDE RACEMASE ACTIVITY AND NUCLEIC ACIDS ENCODING THE SAME				
JOURNAL	Patent: WO 2003106691-A 13 24-DEC-2003;				
FEATURES	DSM IP Assets B.V. (NL)				
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Qy	1	GTTCAGCTTTTKTRTACNAAGTSGB 25			
Db	37	GTTCAGCTTTCTTGTTACAAAGTGGT 13			
RESULT 10					
LOCUS	BD263460	102 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Compositions and methods for use in recombinational cloning of nucleic acids.				
ACCESSION	BD263460				
VERSION	BD263460.1	GI:33073228			
KEYWORDS	JP 2002537790-A/238.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
	artificial sequences.				
REFERENCE	1	(bases 1 to 102)			
AUTHORS	Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.				
TITLE	Compositions and methods for use in recombinational cloning of nucleic acids				
JOURNAL	Patent: JP 2002537790-A 238 12-NOV-2002;				
COMMENT	INVITROGEN CORP				
	OS Artificial Sequence				
	FN JP 2002537790-A/238				
	FD 12-NOV-2002				
	PR 02-MAR-2000 JP 2000602252				
	PF 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR				
	28-MAY-1999 US 60/136744				
	PI JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DAVID CHEO PC				
	CI C12N15/09, C07K14/00, C12N1/19, C12N1/21, C12N5/10, C12N15/00, C12N5/00				
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Db 17 GTTCAGCTTCTTGTCACAAAGTGGT 41

RESULT 11
BD263462      102 bp DNA linear PAT 17-JUL-2003
LOCUS      Compositions and methods for use in recombinational cloning of
DEFINITION nucleic acids.
ACCESSION BD263462.1 GI:33073230
VERSION JP 2002537790-A/240.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 102)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 240 12-NOV-2002;
INVITROGEN CORP
COMMENT OS Artificial Sequence
PN JP 2002537790-A/240
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
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QY 1 GTTCAGCTTTTKRTACNAAGTSGB 25
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Db 14 GTTCAGCTTCTTGTCACAAAGTGGT 38

RESULT 12
BD263228      135 bp DNA linear PAT 17-JUL-2003
LOCUS      Compositions and methods for use in recombinational cloning of
DEFINITION nucleic acids.
ACCESSION BD263228.1 GI:33072996
VERSION JP 2002537790-A/6.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 135)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 6 12-NOV-2002;
INVITROGEN CORP
COMMENT OS Artificial Sequence
PN JP 2002537790-A/6
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
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Db          56 GTTCAGCTTCTCTGTACAAAGTGGT 80
RESULT 14
BD263433
LOCUS      204 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
            nucleic acids.
ACCESSION  BD263433
VERSION    BD263433.1 GI:33073201
KEYWORDS  JP 2002537790-A/211.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE  1 (bases 1 to 204)
AUTHORS   Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE     Compositions and methods for use in recombinational cloning of
            nucleic acids
JOURNAL   Patent: JP 2002537790-A 211 12-NOV-2002;
COMMENT   INVITROGEN CORP
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          PD 12-NOV-2002
          PF 02-MAR-2000 JP 2000602252
          PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
          28-MAY-1999 US 60/136744
          PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
            C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N5/10,C12N15/ PC
            00,C12N5/00
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Best Local Similarity 76.0%; Pred. No. 6.3;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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Db 13 GTTCAGCTTCTCTGTACAAAGTGGT 37

RESULT 15
BD263435
LOCUS      255 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
            nucleic acids.
ACCESSION  BD263435
VERSION    BD263435.1 GI:33073203
KEYWORDS  JP 2002537790-A/213.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE  1 (bases 1 to 255)
AUTHORS   Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE     Compositions and methods for use in recombinational cloning of
            nucleic acids
JOURNAL   Patent: JP 2002537790-A 213 12-NOV-2002;
COMMENT   INVITROGEN CORP
          PN JP 2002537790-A/213
          PD 12-NOV-2002
          PF 02-MAR-2000 JP 2000602252
          PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
          28-MAY-1999 US 60/136744
          PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
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C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N5/10,C12N15/10,C12N15/ PC
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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782.095 Million cell updates/sec

Title: US-10-820-133-5

Perfect score: 25

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.6	86.4	25	2	AAT48214
2	21.6	86.4	25	2	AAX78945
3	21.6	86.4	25	2	AAX78939
4	21.6	86.4	25	4	AAS06185
5	21.6	86.4	25	4	AAC87870
6	21.6	86.4	25	4	AAF55739
7	21.6	86.4	25	4	AD14433
8	21.6	86.4	25	8	ABT16625
9	21.6	86.4	25	9	ACD28280
10	21.6	86.4	25	9	ACD28480
11	21.6	86.4	25	9	ADA38166
12	21.6	86.4	25	10	AAD60562
13	21.6	86.4	25	10	ABZ58738
14	21.6	86.4	25	10	ACC59582
15	21.6	86.4	25	10	ACD44654
16	21.6	86.4	25	12	ADJ46356
17	21.6	86.4	25	12	ADL93420
18	21.6	86.4	25	12	ADO06650
19	21.6	86.4	25	12	ADQ48458
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ALIGNMENTS

RESULT 1  
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ID AAT48214 standard; DNA; 25 BP.

XX AC AAT48214;

DT 20-OCT-1997 (first entry)

XX DE M-attp1 core region.

XX att recombination site; core region; mutation; enhance; recombination;  
vector; subcloning; regulation; exchange; ss.

XX OS Synthetic.

XX WO9640724-Al.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX PA Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
using recombinant proteins and engineered recombination sites in vitro or  
in vivo.

XX Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The  
core region has at least one engineered mutation that enhances  
recombination in vitro in the formation of a Cointegrate or Product DNA.  
These core regions can be incorporated into novel vector donor DNA  
molecules. The nucleic acids, vectors and methods of the invention are  
used to obtain chimeric nucleic acid using recombination proteins and  
engineered recombination sites in vitro or in vivo. The improved  
specificity, speed and yields of the invention facilitates DNA or RNA  
subcloning, regulation or exchange useful for any related purpose, e.g.

AAC55512 Destinati  
AAC55385 Recombina  
AAC55506 Destinati  
Adf42425 AttR2 nuc  
AAC55463 Destinati  
Ad44626 Gateway t  
AAC55541 attR read  
Adq48539 Viral vec  
Ad27063 Plasmid p  
Adi34682 Nucleotid  
Adl90419 Clostridi  
Adq48540 Viral vec  
Adq48544 Viral vec  
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AAC55491 Destinati  
AAC55483 Destinati  
AAC55454 Destinati  
Abz58765 Destinati  
AAC55471 Destinati  
AAC55456 Destinati

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
CC or modification of transcribed, replicated, isolated or genomic DNA or  
CC RNA

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

## RESULT 2

AAx78945  
ID AAX78945 standard; DNA; 25 BP.

XX AC AAX78945;

XX 17-AUG-1999 (first entry)

XX Oligonucleotide #11 for recombination and cloning method.

XX Cloning; donor; recombination site; vector; chimeric; ss.

XX Synthetic.

XX WO9921977-A1.

XX 06-MAY-1999.

XX 26-OCT-1998; 98WO-US022589.

XX 24-OCT-1997; 97US-0065930P.

XX 23-OCT-1998; 98US-00177387.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Fox DK;

XX WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

XX Disclosure; Page 161; 185pp; English.

PS The invention relates to novel methods for cloning or subcloning one or  
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
CC more desired nucleic acid segments flanked by at least 2 recombination  
CC sites which do not recombine with each other; (2) one or more vector  
CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
CC not recombine with each other; and (3) one or more site-specific  
CC recombination proteins; (b) incubating the combination to transfer one or  
CC more of the desired segments into one or more of the VDMs, thereby  
CC producing one or more desired product molecules (PMs). The methods can be  
CC used for the efficient and specific recombination of NAM segments. They  
CC can be used to generate chimeric DNA or RNA molecules that have the  
CC desired characteristics and/or nucleic acid segments. The methods can  
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
CC are used in the method of the invention

SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 86.4%; Score 21.6; DB 2; Length 25;  
Best Local Similarity 76.0%; Pred. No. 2.2;  
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25  
|||||  
Db 1 GTTCAGCTTCTTGACAAAGTGGT 25

## RESULT 3

AAx78939

ID AAX78939 standard; DNA; 25 BP.

XX AC AAX78939;

XX 17-AUG-1999 (first entry)

XX Oligonucleotide #5 for recombination and cloning method.

XX Cloning; donor; recombination site; vector; chimeric; ss.

XX Synthetic.

XX WO9921977-A1.

XX 06-MAY-1999.

XX 26-OCT-1998; 98WO-US022589.

XX 24-OCT-1997; 97US-0065930P.

XX 23-OCT-1998; 98US-00177387.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Fox DK;

XX WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

XX Disclosure; Page 159; 185pp; English.

PS The invention relates to novel methods for cloning or subcloning one or  
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
CC more desired nucleic acid segments flanked by at least 2 recombination  
CC sites which do not recombine with each other; (2) one or more vector  
CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
CC not recombine with each other; and (3) one or more site-specific  
CC recombination proteins; (b) incubating the combination to transfer one or  
CC more of the desired segments into one or more of the VDMs, thereby  
CC producing one or more desired product molecules (PMs). The methods can be  
CC used for the efficient and specific recombination of NAM segments. They  
CC can be used to generate chimeric DNA or RNA molecules that have the  
CC desired characteristics and/or nucleic acid segments. The methods can  
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
CC are used in the method of the invention

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25  
|||||

Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

## RESULT 4

AAx06185

ID AAS06185 standard; DNA; 25 BP.

XX AC AAS06185;

XX 12-SEP-2001 (first entry)

XX Phage-lambda recombination site attR2.

XX Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;



KW lambda integrase; therapeutic; ss.  
 OS Bacteriophage lambda.  
 XX WO200142509-A1.  
 PN 14-JUN-2001.  
 XX 11-DEC-2000; 2000WO-US033546.  
 PF 10-DEC-1999; 99US-0169983P.  
 XX 09-MAR-2000; 2000US-0188020P.  
 PR (CHEO/) CHEO D.  
 XX (BRAS/) BRASCH M A.  
 PA (TEMP/) TEMPLE G F.  
 PA (HART/) HARTLEY J L.  
 PA (BYRD/) BYRD D R N.  
 XX  
 PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;  
 XX WPI; 2001-356174/37.  
 DR  
 XX Producing hybrid nucleic acids, useful for expressing novel therapeutic  
 PT polypeptides, by mixing the same or different nucleic acids having one or  
 PT more recombination sites in the presence of recombination proteins, e.g.  
 PT Cre.  
 XX  
 PS Disclosure; Fig 24A; 357pp; English.  
 XX  
 CC AAS06174-AAS06322 represent Bacteriophage lambda att recombination site  
 CC nucleic acid sequences, and PCR primers of the invention. The att  
 CC sequences are recognised by the recombination protein lambda integrase  
 CC (Int). The invention is a new method of producing a population of hybrid  
 CC nucleic acids comprising mixing at least a first population of nucleic  
 CC acids comprising one or more recombination sites with at least one target  
 CC nucleic acid comprising one or more recombination sites and causing some  
 CC or all of the nucleic acids to recombine with all or some of the target  
 CC nucleic acids. The method is useful for producing a population of hybrid  
 CC nucleic acids which may be the same or different. The nucleic acids may  
 CC be used to express therapeutic proteins or peptides and they may also be  
 CC used to create novel fusion proteins by expressing different sequences  
 CC linked to each other. The method allows simultaneous cloning of two or  
 CC more different nucleic acids  
 XX  
 SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;  
 Query Match 86.4%; Score 21.6; DB 4; Length 25;  
 Best Local Similarity 76.0%; Pred. No. 2.2;  
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 GTTCAGCTTTTKTRTACNAAGTSGB 25  
 DB 1 GTTCAGCTTTCTGTACAAAGTGGT 25  
 RESULT 5  
 AAC87870  
 ID AAC87870 standard; DNA; 25 BP.  
 XX AAC87870;  
 AC  
 XX 02-MAR-2001 (first entry)  
 DT  
 XX Escherichia coli core region recombinant site m-attP1 SEQ ID NO:5.  
 DE  
 XX Core region; recombination site; cloning; chimeric DNA; characteristic;  
 KW mutation; att site; lox site; ss.  
 XX Escherichia coli.  
 OS  
 XX US6143557-A.  
 PN  
 XX

PD 07-NOV-2000.  
 XX 20-JAN-1999; 99US-00233493.  
 PF 07-JUN-1995; 95US-00486139.  
 XX 07-JUN-1996; 96US-00663002.  
 PR 12-JAN-1998; 98US-00005476.  
 XX (LIFE-) LIFE TECHNOLOGIES INC.  
 PA Brasch MA, Hartley JL;  
 XX WPI; 2001-049004/06.  
 DR  
 XX Isolated nucleic acid molecules comprising a DNA segment having two  
 PT engineered recombination sites, derived from att or lox, which flank a  
 PT selectable marker and comprise a core region having an engineered  
 PT mutation.  
 XX  
 PS Claim 1; Col 18; 73pp; English.  
 XX  
 CC The present invention describes an isolated nucleic acid molecule (I)  
 CC comprising a first nucleic acid sequence having a defined sequence  
 CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,  
 CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described  
 CC are: (1) an isolated nucleic acid molecule (II) comprising a first  
 CC mutated recombination site that removes one or more stop codons from the  
 CC recombination site or avoids hairpin formation, the recombination site  
 CC being an att or lox site; (2) an isolated nucleic acid molecule (III)  
 CC comprising a first att recombination site comprising a mutation that  
 CC enhances recombination specificity; (3) vectors (IV) comprising the above  
 CC mentioned nucleic acids; and (4) cells comprising the above mentioned  
 CC nucleic acids or (IV). The nucleic acids are used in engineering a core  
 CC region of a given recombination site to provide mutative sites suitable  
 CC for subcloning reactions. The use of nucleic acids for obtaining  
 CC engineered recombination in vitro or in vivo makes the methods for DNA or  
 CC RNA subcloning, highly specific, rapid, and less labour intensive  
 XX  
 SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;  
 Query Match 86.4%; Score 21.6; DB 4; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GTTCAGCTTTTKTRTACNAAGTSGB 25  
 DB 1 GTTCAGCTTTTKTRTACNAAGTSGB 25  
 RESULT 6  
 AAF55739  
 ID AAF55739 standard; DNA; 25 BP.  
 XX AAF55739;  
 AC  
 XX 12-APR-2001 (first entry)  
 DT  
 XX Recombination site m-attP1.  
 DE  
 XX Recombination site; cloning; m-att; ss.  
 KW  
 XX Unidentified.  
 OS  
 XX US6171861-B1.  
 PN  
 XX 09-JAN-2001.  
 PD  
 XX 12-JAN-1998; 98US-00005476.  
 PF  
 XX 07-JUN-1995; 95US-00486139.  
 PR 07-JUN-1996; 96US-00663002.  
 XX (LIFE-) LIFE TECHNOLOGIES INC.  
 PA

XX PI Hartley JL, Brasch MA;  
 XX WPI; 2001-136877/14.  
 XX  
 PT In vitro cloning of nucleic acid involves mixing vectors comprising  
 PT recombination sites and/or nucleic acid, incubating mixture to produce  
 PT chimeric molecule, contacting hosts with mixture and selecting host.  
 XX PS Claim 24; Col 46; 73pp; English.  
 XX  
 CC The present invention relates to a method for in vitro cloning of a  
 CC nucleic acid of interest. The method involves mixing in vitro two vectors  
 CC each comprising at least one recombination site and the nucleic acid of  
 CC interest; incubating the mixture in the presence of at least one  
 CC recombination protein to result in recombination of the recombination  
 CC sites, leading to production of a chimeric nucleic acid molecule  
 CC comprising the nucleic acid of interest; contacting hosts with the  
 CC mixture; and selecting for a host comprising the chimeric nucleic acid  
 CC molecule, and selecting against a host comprising the vectors comprising  
 CC the second vector, to clone the nucleic acid. The present sequence is a  
 CC recombination site, which may be used in the method of the present  
 CC invention  
 XX  
 SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;  
 Query Match 86.4%; Score 21.6; DB 4; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTTCAGCTTYYKTRTACNAAAGTSG 25  
 |||||  
 DB 1 GTTCAGCTTYYKTRTACNAAAGTSG 25  
 |||||  
 RESULT 7  
 AAD14433  
 ID AAD14433 standard; DNA; 25 BP.  
 XX  
 AC AAD14433;  
 DT 01-NOV-2001 (first entry)  
 DE Recombination site m-attP1 DNA.  
 XX  
 KW Recombination site; copy number; replicon; recombinatorial cloning;  
 KW m-attP1; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN US6270969-B1.  
 XX  
 PD 07-AUG-2001.  
 XX  
 PF 20-JAN-1999; 99US-00233492.  
 XX  
 PR 07-JUN-1995; 95US-00486139.  
 PR 07-JUN-1996; 96US-00663002.  
 XX  
 PA (INVI-) INVITROGEN CORP.  
 XX  
 PI Hartley JL, Brasch MA;  
 XX  
 DR WPI; 2001-488248/53.  
 XX  
 PT Methods for apposing nucleic acids comprising an expression signal and a  
 PT gene/partial gene, using recombinatorial cloning by incubating the  
 PT nucleic acids in the presence of a recombination protein under conditions  
 PT for recombination.  
 XX  
 PS Claim 14; Col 18; 76pp; English.  
 XX  
 CC The invention relates to a method for apposing an expression signal and a

CC gene or partial gene, using recombinatorial cloning. The method incubates  
 CC nucleic acids comprising the expression signal and the gene/partial gene  
 CC in the presence of a recombination protein under conditions sufficient to  
 CC cause recombination and therefore appose the expression signal and the  
 CC gene or partial gene. The methods are useful for apposing an expression  
 CC signal and a gene or partial gene using recombinatorial cloning. The  
 CC methods are also useful for changing vectors, constructing genes for  
 CC fusion proteins, changing copy number, changing replicons, cloning into  
 CC phages, and cloning e.g., PCR products (with an attB site at one end and  
 CC a loxp site at the other end), genomic DNAs, and cDNAs. The methods are  
 CC highly specific, rapid, and less labour intensive than prior art methods.  
 CC The present sequence is a recombination site useful for recombination  
 CC cloning  
 XX  
 SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;  
 Query Match 86.4%; Score 21.6; DB 4; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTTCAGCTTYYKTRTACNAAAGTSG 25  
 |||||  
 DB 1 GTTCAGCTTYYKTRTACNAAAGTSG 25  
 |||||  
 RESULT 8  
 ABT16625  
 ID ABT16625 standard; DNA; 25 BP.  
 XX  
 AC ABT16625;  
 DT 03-APR-2003 (first entry)  
 DE Artificial plant chromosome related oligo SEQ ID No 37.  
 XX  
 KW Plant artificial chromosome; PAC; transgenic plant; vaccine;  
 KW blood factor; herbicide; stress; agronomical; nutrient quality;  
 KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;  
 KW ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200296923-A1.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-US017451.  
 XX  
 PR 30-MAY-2001; 2001US-0294687P.  
 PR 04-JUN-2001; 2001US-0296329P.  
 XX  
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.  
 PA (AGRI-) AGRISOMA INC.  
 XX  
 PI Perez C, Fabijanski SF, Perkins E;  
 XX  
 DR WPI; 2003-140436/13.  
 XX  
 PT Producing artificial chromosome by introducing a nucleic acid into plant  
 PT cell, selecting artificial chromosome that has one or more repeat regions  
 PT with equivalent amounts of euchromatic and heterochromatic nucleic acids.  
 XX  
 PS Disclosure; Page 262; 269pp; English.  
 XX  
 CC The invention relates to a novel method for producing plant artificial  
 CC chromosomes. The invention also relates to methods for targeting  
 CC insertion of heterologous DNA into plant artificial chromosomes, methods  
 CC for delivery of plant chromosomes to selected cells and tissues. The  
 CC isolated plant artificial chromosome (PAC) is useful for producing a  
 CC transgenic plant, which involves introducing the PAC into a plant cell.  
 CC The PAC comprises a heterologous nucleic acid encoding a gene product  
 CC such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker  
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and

CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,  
 CC cytokines, growth factors, antibodies, or a product that provides for  
 CC resistance to diseases, insects, herbicides, or stress in a plant. The  
 CC heterologous nucleic acid optionally encodes a product that provides an  
 CC agronomically important trait in the plant, e.g. a product that alters  
 CC nutrient use and/or improves the nutrient quality of the plant. The  
 CC heterologous nucleic acid is contained within a bacterial artificial  
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This  
 CC polynucleotide sequence represents an oligo relating to the method for  
 CC producing plant artificial chromosomes of the invention

XX SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 8; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKTACNAAGTSGB 25

Db 1 GTTCAGCTTTTKTACNAAGTSGB 25

# RESULT 9

ID ACD28280 standard; DNA; 25 BP.

XX AC ACD28280;

XX DT 02-OCT-2003 (first entry)

XX DE Nucleic acid core region m-attP1.

XX KW Core region; ds; vector donor DNA; flanking recombination site; m-attP1.

XX OS Synthetic.

XX PN US2003064515-A1.

XX PD 03-APR-2003.

XX PF 30-JAN-2002; 2002US-00058291.

XX PR 07-JUN-1995; 95US-00486139.

XX PR 07-JUN-1996; 96US-00663002.

XX PR 20-JAN-1999; 99US-00233493.

XX PR 02-NOV-1999; 99US-00432085.

XX PA (HARTLEY) HARTLEY J L.

XX PA (BRASCH) BRASCH M A.

XX PI Hartley JL, Brasch MA;

XX DR WPI; 2003-540791/51.

XX PT New Vector Donor DNA molecule for recombinational cloning using

XX PT engineered recombination sites, comprises first and second DNA segments

XX PT that do not recombine with each other and that contain a Selectable

XX PT marker.

XX PS Claim 14; Page 25; 71pp; English.

XX CC The invention relates to a vector donor DNA molecule comprising a first

XX CC DNA segment and a second DNA segment containing at least one selectable

XX CC marker. The first and second segments are separated either by, in a

XX CC circular vector donor, a first and a second recombination site, or in a

XX CC linear vector donor, at least a first recombination site, where each pair

XX CC of flanking recombination sites are engineered and do not recombine with

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKTACNAAGTSGB 25

Db 1 GTTCAGCTTTTKTACNAAGTSGB 25

# RESULT 10

ACD28480

ID ACD28480 standard; DNA; 25 BP.

XX AC ACD28480;

XX DT 09-OCT-2003 (first entry)

XX DE Nucleic acid core sequence m-attP1.

XX KW Nucleic acid core; m-attP1; cointegrate DNA; flanking recombination site;  
 XX ds.

XX OS Synthetic.

XX PN US2003068799-A1.

XX PD 10-APR-2003.

XX PF 06-JUN-2002; 2002US-00162879.

XX PR 07-JUN-1995; 95US-00486139.

XX PR 07-JUN-1996; 96US-00663002.

XX PR 20-JAN-1999; 99US-00233493.

XX PR 02-NOV-1999; 99US-00432085.

XX PA (INVI-) INVITROGEN CORP.

XX PI Hartley JL, Brasch MA;

XX DR WPI; 2003-540884/51.

XX PT Making CoIntegrate DNA molecule, by combining recombination sites

XX PT flanking the desired DNA segment in insert donor DNA, with the

XX PT recombination sites of vector donor DNA, using site specific

XX PT recombination protein.

XX PS Claim 14; Page 25; 71pp; English.

XX CC The invention relates to a method of making a coIntegrate DNA molecule.  
 XX CC The method is useful for making a coIntegrate DNA molecule. The method is  
 XX CC useful for a variety of DNA exchanges, such as subcloning of DNA, in  
 XX CC vitro or in vivo. The method enables efficient and specific recombination  
 XX CC of DNA segments using recombination proteins. The method is highly  
 XX CC specific, rapid and less labour intensive. The improved specificity,  
 XX CC yield and speed of the method facilitates DNA or RNA subcloning,  
 XX CC regulation and exchange useful for other related purposes. Since single  
 XX CC molecules of the recombinations product can be introduced into a  
 XX CC biological host, propagation of the desired product DNA in the absence of  
 XX CC other DNA molecules is more readily realised. Reaction conditions can be  
 XX CC freely adjusted in vitro to optimise enzyme activities. The present  
 XX CC sequence represents the nucleic acid core sequence m-attP1

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKTACNAAGTSGB 25

Db 1 GTTCAGCTTTTKTACNAAGTSGB 25

```

RESULT 11
ADA38166
ID ADA38166 standard; DNA; 25 BP.
XX
AC ADA38166;
XX
DT 20-NOV-2003 (first entry)
XX
DE m-attP1 DNA sequence indicating generic core region of an attP1 site.
XX
KW engineered recombination site; cloning; recombinase; subcloning; attB;
KW attP; attL; attR; selectable marker; cointegrate; m-attP1; ds.
XX
OS Synthetic.
XX
PN US2003054552-A1.
XX
PD 20-MAR-2003.
XX
PF 30-JAN-2002; 2002US-00058292.
XX
PR 07-JUN-1995; 95US-00486139.
PR 07-JUN-1996; 96US-00663002.
PR 20-JAN-1999; 99US-00233493.
PR 02-NOV-1999; 99US-00432085.
XX
PA (HART/) HARTLEY J L.
PA (BRAS/) BRASCH M A.
XX
PI Hartley JL, Brasch MA;
XX
DR WPI; 2003-585168/55.
XX
PS Claim 14; Page 26; 72pp; English.
XX
CC This invention relates to novel DNA and vectors having engineered
CC recombination sites for use in a cloning method that enables efficient
CC and specific recombination of DNA segments using recombination proteins
CC including recombinases. As such, it provides a method for obtaining
CC chimeric nucleic acids with the desired characteristics, facilitating DNA
CC or RNA subcloning, regulation and/or exchange. The recombination site is
CC derived from attB attP, attL or attR, where the att site is att1, att2 or
CC att3. Engineered mutations of the att sites (either one or multiple
CC mutations) can enhance specificity or efficiency of the recombination
CC reaction and the properties of the product DNA molecules. Accordingly,
CC the present invention describes a nucleic acid molecule comprising at
CC least one DNA segment having at least two engineered recombination sites
CC flanking a selectable marker and/or a desired DNA segment. Furthermore,
CC at least one of the engineered sites must enhance recombination in vitro
CC to form a cointegrate or product DNA molecule. This oligonucleotide
CC sequence is m-attP1, a generic DNA sequence indicating the core region of
CC an attP1 recombination site of the invention.
XX
SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKRTACNAAGTSGB 25
Db 1 GTTCAGCTTTTKRTACNAAGTSGB 25

RESULT 12
AAD60562
ID AAD60562 standard; DNA; 25 BP.
XX
AC AAD60562;
XX
DT 18-DEC-2003 (first entry)
XX
DE Core region DNA, m-attP1.
XX
KW Recombinational cloning; DNA exchange; core region; ds.
XX
OS Unidentified.
XX
PN US2003100110-A1.
XX
PD 29-MAY-2003.
XX
PF 02-NOV-1999; 99US-00432085.
XX
PR 07-JUN-1995; 95US-00486139.
PR 07-JUN-1996; 96US-00663002.
PR 20-JAN-1999; 99US-00233493.
XX
PA (HART/) HARTLEY J L.
PA (BRAS/) BRASCH M A.
XX
PI Hartley JL, Brasch MA;
XX
DR WPI; 2003-730143/69.
XX
PS Claim 14; Page 25; 71pp; English.
XX
CC The invention relates to a vector donor DNA molecule which comprises
CC first and second DNA segments that do not recombine with each other and
CC that contain a selectable marker. The invention also relates to a method
CC for recombinational cloning using engineered recombination sites. The
CC invention is useful for moving or exchanging segments of DNA molecules
CC using engineered recombination sites and recombination proteins to
CC provide chimeric DNA molecules that have the desired characteristic(s)
CC and/or DNA segment(s). The present sequence is a core region DNA. This
CC sequence is used to illustrate the method of the invention
XX
SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKRTACNAAGTSGB 25
Db 1 GTTCAGCTTTTKRTACNAAGTSGB 25

RESULT 13
ABZ58738
ID ABZ58738 standard; DNA; 25 BP.
XX
AC ABZ58738;
XX
DT 01-MAY-2003 (first entry)
XX
DE Att site nucleotide sequence attR2.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; att; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.

```

XX 28-NOV-2002.  
XX 21-MAY-2002; 2002WO-US015947.  
XX 21-MAY-2001; 2001US-0291973P.  
XX (INVI-) INVITROGEN CORP.  
XX Braach MA, Cheo D, Li X, Eposito D, Byrd DRN;  
XX WPI; 2003-129436/12.  
XX Inserting a population of nucleic acids into a second target molecule for  
XX selecting and isolating nucleic acid molecules by mixing the second  
XX population of nucleic acid with a second target nucleic acid.  
XX Disclosure; Fig 13A; 273pp; English.  
XX The invention relates to inserting a population of nucleic acids into a  
XX second target molecule. The method involves (a) mixing a first population  
XX of nucleic acid comprising one or more recombination sites with a target  
XX nucleic acid; (b) causing some or all of the nucleic acid molecules of  
XX the first population to recombine with the first target nucleic acid  
XX molecules to form a second population; (c) mixing the second population  
XX of nucleic acid with a second target nucleic acid; and (d) causing some  
XX or all of the nucleic acid molecules of the second population to  
XX recombine with some or all of the second target nucleic acid molecules to  
XX form a third population of nucleic acid. The method is useful for  
XX selecting and isolating nucleic acid molecules. Sequences ABZ58727-762  
XX represent att recombination site sequences used in the method of the  
XX invention  
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;  
XX  
XX Query Match 86.4%; Score 21.6; DB 10; Length 25;  
XX Best Local Similarity 76.0%; Pred. No. 2.2;  
XX Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
OY 1 GTTCAGCTTTVKTACNAAGTSGB 25  
DB 1 GTTCAGCTTTCTGTACAAAGTGGT 25  
XXXXXXXXXXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXXXXXXXXXXXXXXXXXXXX  
RESULT 14  
ACC59582  
ID ACC59582 standard; DNA; 25 BP.  
XX  
XX ACC59582;  
XX  
XX 08-SEP-2003 (first entry)  
XX Nucleic acid preparation method att site SEQ ID NO: 30.  
XX Nucleic acid preparation; cloning; mutagenesis; adaptor; cleavage site;  
XX genetic engineering; PCR; primer; adaptor; ss.  
XX Bacteriophage lambda.  
XX  
XX WO200304207-A2.  
XX  
XX 30-MAY-2003.  
XX  
XX 22-NOV-2002; 2002WO-IB005316.  
XX  
XX 22-NOV-2001; 2001JP-00357821.  
XX  
XX (INVI-) INVITROGEN JAPAN KK.  
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
XX Nomura N, Goshima N, Kisu Y, Sono S;  
XX WPI; 2003-457615/43.

XX Preparing nucleic acids for genetic analyses comprises contacting a  
XX template nucleic acid molecule with a primer and a polypeptide having DNA  
XX polymerase activity to form a mixture, and incubating the mixture to  
XX extend the primer.  
XX Disclosure; Page 36; 81pp; English.  
XX The present invention relates to a method of preparing nucleic acid  
XX molecules, which comprises contacting a template nucleic acid molecule  
XX with a first, second and third primer and a polypeptide with DNA  
XX polymerase activity to form a mixture and incubating the mixture to  
XX extend the primers. The method is useful in genetic engineering,  
XX particularly in the amplification, rapid cloning and mutagenesis of  
XX nucleic acid molecules for genetic analyses. The present sequence is an  
XX oligonucleotide shown in the exemplification of the invention  
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;  
XX  
XX Query Match 86.4%; Score 21.6; DB 10; Length 25;  
XX Best Local Similarity 76.0%; Pred. No. 2.2;  
XX Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
OY 1 GTTCAGCTTTVKTACNAAGTSGB 25  
DB 1 GTTCAGCTTTCTGTACAAAGTGGT 25  
XXXXXXXXXXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXXXXXXXXXXXXXXXXXXXX  
RESULT 15  
ACC44654  
ID ACC44654 standard; DNA; 25 BP.  
XX  
XX ACC44654;  
XX  
XX 29-MAY-2003 (first entry)  
XX Recombination site related oligonucleotide SEQ ID NO:45.  
XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;  
XX att site; integrase; recombinase; ACes; gene therapy; transgenic animal;  
XX platform artificial chromosome expression system; PCR primer; ss.  
XX Synthetic.  
XX  
XX WO200297059-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 30-MAY-2002; 2002WO-US017452.  
XX  
XX 30-MAY-2001; 2001US-0294758P.  
XX 21-MAR-2002; 2002US-0366891P.  
XX  
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.  
XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;  
XX Stewart S, Shellard J;  
XX WPI; 2003-140461/13.  
XX Novel eukaryotic chromosome comprising one or many att sites which  
XX permits site-directed integration in the presence of lambda-integrase,  
XX useful for site-specific recombination-directed integration of DNA of  
XX interest.  
XX Claim 43; Page 143; 272pp; English.  
XX The present invention describes a eukaryotic chromosome (I) comprising  
XX one or several att sites, where an att site is heterologous to the  
XX chromosome, and permits site-directed integration in the presence of  
XX lambda-integrase. Also described: (1) a platform artificial chromosome  
XX expression system (ACes) (II) comprising several sites that participate  
XX in recombinase catalysed recombination; and (2) a method (M1) for

CC introducing a heterologous nucleic acid into a platform artificial  
CC chromosome. (I) can be used in gene therapy. (M1) is useful for  
CC introducing a heterologous nucleic acid molecule into a platform  
CC artificial chromosome, preferably an ACes. (II) is useful for producing a  
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or  
CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection  
CC by a carrier system, microinjection, microcell fusion, electroporation,  
CC microprojectile bombardment or direct DNA transfer into an embryonic  
CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous  
CC nucleic acid that encodes a therapeutic product which is useful for  
CC making a library of ACes comprising random portions of a genome. ACC44612  
CC to ACC4732 and ABP9650 to ABP9657 represent sequences used in the  
CC exemplification of the present invention  
XX

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

Search completed: November 16, 2004, 04:02:48  
Job time : 168.8 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds  
(without alignments)  
494.978 Million cell updates/sec

Title: US-10-820-133-5

Perfect score: 25

Sequence: 1 gttcagcttcttctacnaagtsb 25

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.6	86.4	25	3	US-09-233-493-5
2	21.6	86.4	25	3	US-09-005-476-5
3	21.6	86.4	25	3	US-09-233-492-5
4	21.6	86.4	25	3	US-09-296-280-5
5	21.6	86.4	25	3	US-09-296-280-11
6	21.6	86.4	25	4	US-09-498-074-5
7	21.6	86.4	25	4	US-09-498-074-5
8	21.6	86.4	25	5	PCT-US96-10082A-5
9	21.2	84.8	25	3	US-09-296-280-42
10	20.4	81.6	25	3	US-09-233-493-11
11	20.4	81.6	25	3	US-09-233-493-15
12	20.4	81.6	25	3	US-09-233-493-16
13	20.4	81.6	25	3	US-09-005-476-11
14	20.4	81.6	25	3	US-09-005-476-15
15	20.4	81.6	25	3	US-09-005-476-16
16	20.4	81.6	25	3	US-09-233-492-11
17	20.4	81.6	25	3	US-09-233-492-15
18	20.4	81.6	25	3	US-09-233-492-16
19	20.4	81.6	25	3	US-09-296-280-15
20	20.4	81.6	25	3	US-09-296-280-16
21	20.4	81.6	25	3	US-09-296-280-43
22	20.4	81.6	25	4	US-09-498-074-11
23	20.4	81.6	25	4	US-09-498-074-15
24	20.4	81.6	25	4	US-09-498-074-16
25	20.4	81.6	25	4	US-09-498-074-11
26	20.4	81.6	25	4	US-09-498-074-15
27	20.4	81.6	25	4	US-09-498-074-16

28	20.4	81.6	25	5	PCT-US96-10082A-11	Sequence 11, Appl
29	20.4	81.6	25	5	PCT-US96-10082A-15	Sequence 15, Appl
30	20.4	81.6	25	5	PCT-US96-10082A-16	Sequence 16, Appl
31	20.4	81.6	201	1	US-08-021-667A-18	Sequence 18, Appl
32	20.4	81.6	201	1	US-08-410-544-18	Sequence 18, Appl
33	20.4	81.6	201	1	US-08-728-785A-18	Sequence 18, Appl
34	20.4	81.6	1763	4	US-09-244-805-57	Sequence 57, Appl
35	20.4	81.6	4909	3	US-08-556-978B-78	Sequence 78, Appl
36	20.4	81.6	6043	4	US-09-630-929-4	Sequence 4, Appl
37	20.4	81.6	7652	1	US-07-590-988A-1	Sequence 1, Appl
38	20	80.0	25	3	US-09-233-493-3	Sequence 3, Appl
39	20	80.0	25	3	US-09-005-476-3	Sequence 3, Appl
40	20	80.0	25	3	US-09-233-492-3	Sequence 3, Appl
41	20	80.0	25	3	US-09-296-280-3	Sequence 3, Appl
42	20	80.0	25	4	US-09-498-074-3	Sequence 3, Appl
43	20	80.0	25	4	US-09-498-074-3	Sequence 3, Appl
44	20	80.0	25	5	PCT-US96-10082A-3	Sequence 3, Appl
45	19.6	78.4	25	3	US-09-233-493-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-09-233-493-5  
; Sequence 5, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
US-09-233-493-5

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Query Match      86.4%; Score 21.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25
    |||||
Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

RESULT 2
US-09-005-476-5
; Sequence 5, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-5

Query Match      86.4%; Score 21.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25
    |||||
Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

RESULT 3
US-09-233-492-5
; Sequence 5, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
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; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-5

Query Match      86.4%; Score 21.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25
    |||||
Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

RESULT 4
US-09-296-280-5
; Sequence 5, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942,2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-5
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Query Match 86.4%; Score 21.6; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0;

Oy 1 GTTCAGCTTTTKTACNAAGTSG 25  
|||||  
Db 1 GTTCAGCTTTTKTACNAAGTSG 25

## RESULT 5

US-09-296-280-11  
; Sequence 11, Application US/09296280  
; Patent No. 6277608  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850007  
; CURRENT APPLICATION NUMBER: US/09/296.280  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: US 09/177,387  
; EARLIER FILING DATE: 1998-10-23  
; EARLIER APPLICATION NUMBER: US 60/065,930  
; EARLIER FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-296-280-11

Query Match 86.4%; Score 21.6; DB 3; Length 25;  
Best Local Similarity 76.0%; Pred. No. 0.3;  
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTTTKTACNAAGTSG 25  
|||||  
Db 1 GTTCAGCTTTCTGTACAAAGTGT 25

## RESULT 6

US-09-498-074-5  
; Sequence 5, Application US/09498074  
; Patent No. 6534264  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/498,074  
; FILING DATE: (Herewith)  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
US-09-498-074-5

Query Match 86.4%; Score 21.6; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0;

Oy 1 GTTCAGCTTTTKTACNAAGTSG 25  
|||||  
Db 1 GTTCAGCTTTTKTACNAAGTSG 25

## RESULT 7

US-09-498-074-5  
; Sequence 5, Application US/09498074  
; Patent No. 6720140  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/498,074  
; FILING DATE: 04-Feb-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid

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;
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-498-074-5

Query Match      86.4%; Score 21.6; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKRTACNAAGTSGB 25
Db 1 GTTCAGCTTTTKRTACNAAGTSGB 25

RESULT 8
PCT-US96-10082A-5
; Sequence 5, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
PCT-US96-10082A-5

Query Match      86.4%; Score 21.6; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKRTACNAAGTSGB 25
Db 1 GTTCAGCTTTTKRTACNAAGTSGB 25

RESULT 9
US-09-296-280-42
; Sequence 42, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
```

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;
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296.280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-42

Query Match      84.8%; Score 21.2; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.46;
Matches 20; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKRTACNAAGTSGB 25
Db 1 GTTCAGCTTTTKRTACNAAGTSGB 25

RESULT 10
US-09-233-493-11
; Sequence 11, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-11

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTXYKTRTACNAAGTSG 25
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Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 11
US-09-233-493-15
; Sequence 15, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233.493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-15

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTXYKTRTACNAAGTSG 25
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Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 12
US-09-233-493-16
; Sequence 16, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233.493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-16

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTXYKTRTACNAAGTSG 25
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Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 13
US-09-005-476-11
; Sequence 11, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
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; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-11

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GTTCAGCTTTTKRTACNAAGTSG 25
Db      1 GTTCAGCTTTCTGTACAAAGTTGG 25

RESULT 14
US-09-005-476-15
; Sequence 15, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-15

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GTTCAGCTTTTKRTACNAAGTSG 25
Db      1 GTTCAGCTTTCTGTACAAAGTTGG 25

RESULT 15
US-09-005-476-16
; Sequence 16, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-16

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GTTCAGCTTTTKRTACNAAGTSG 25
Db      1 GTTCAGCTTTCTGTACAAAGTTGG 25

Search completed: November 16, 2004, 10:22:31
Job time : 36.9 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 ; Search time 314 Seconds  
(without alignments)  
430.015 Million cell updates/sec

Title: US-10-820-133-5

Perfect score: 25

Sequence: 1 gttcagcttcttctacnaagtsb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Published Applications NA: \*
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  - 2: /cgn2\_6/ptodata/1/pubna/PCT\_NEW\_PUB.seq.\*
  - 3: /cgn2\_6/ptodata/1/pubna/US06\_NEW\_PUB.seq.\*
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  - 11: /cgn2\_6/ptodata/1/pubna/US09C\_PUBCOMB.seq.\*
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  - 19: /cgn2\_6/ptodata/1/pubna/US11\_NEW\_PUB.seq.\*
  - 20: /cgn2\_6/ptodata/1/pubna/US60\_NEW\_PUB.seq.\*
  - 21: /cgn2\_6/ptodata/1/pubna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	21.6	86.4	25	US-09-732-914-12
2	21.6	86.4	25	US-09-855-797A-5
3	21.6	86.4	25	US-09-855-797A-11
4	21.6	86.4	25	US-09-907-900-5
5	21.6	86.4	25	US-09-907-900-11
6	21.6	86.4	25	US-09-907-719-5
7	21.6	86.4	25	US-09-907-719-11
8	21.6	86.4	25	US-09-432-085-5
9	21.6	86.4	25	US-09-985-448-5
10	21.6	86.4	25	US-09-985-448-11
11	21.6	86.4	25	US-10-058-292-5
12	21.6	86.4	25	US-10-058-291-5

13	21.6	86.4	25	14	US-10-162-879-5	Sequence 5, Appli
14	21.6	86.4	25	15	US-10-161-403-45	Sequence 45, Appli
15	21.6	86.4	25	15	US-10-151-690-36	Sequence 36, Appli
16	21.6	86.4	25	15	US-10-300-892-5	Sequence 5, Appli
17	21.6	86.4	25	15	US-10-300-892-11	Sequence 11, Appli
18	21.6	86.4	25	16	US-10-301-849A-30	Sequence 30, Appli
19	21.6	86.4	25	16	US-10-680-316-5	Sequence 5, Appli
20	21.6	86.4	25	16	US-10-680-316-11	Sequence 11, Appli
21	21.6	86.4	25	17	US-10-815-730-5	Sequence 5, Appli
22	21.6	86.4	25	17	US-10-815-730-11	Sequence 11, Appli
23	21.6	86.4	25	17	US-10-820-133-5	Sequence 5, Appli
24	21.6	86.4	25	17	US-10-820-133-11	Sequence 11, Appli
25	21.6	86.4	25	18	US-10-161-408-37	Sequence 37, Appli
26	21.6	86.4	25	18	US-10-622-088-18	Sequence 18, Appli
27	21.6	86.4	25	18	US-10-622-088-5	Sequence 5, Appli
28	21.6	86.4	158	15	US-10-403-232-183	Sequence 183, App
29	21.6	86.4	1846	15	US-10-023-208-63	Sequence 63, Appli
30	21.6	86.4	5038	18	US-10-622-088-89	Sequence 89, Appli
31	21.6	86.4	5148	11	US-09-860-763-10	Sequence 10, Appli
32	21.6	86.4	5375	17	US-10-612-410-5	Sequence 5, Appli
33	21.6	86.4	5558	15	US-10-241-596-137	Sequence 137, App
34	21.6	86.4	5693	18	US-10-622-088-90	Sequence 90, Appli
35	21.6	86.4	5763	18	US-10-622-088-94	Sequence 94, Appli
36	21.6	86.4	6464	15	US-10-151-690-20	Sequence 20, Appli
37	21.6	86.4	6959	17	US-10-612-410-3	Sequence 3, Appli
38	21.6	86.4	7278	16	US-10-097-034A-37	Sequence 37, Appli
39	21.6	86.4	7341	18	US-10-622-088-112	Sequence 112, App
40	21.6	86.4	7618	17	US-10-612-410-1	Sequence 1, Appli
41	21.6	86.4	7995	18	US-10-622-088-113	Sequence 113, App
42	21.6	86.4	8599	18	US-10-622-088-115	Sequence 115, App
43	21.6	86.4	8634	18	US-10-632-088-107	Sequence 107, App
44	21.6	86.4	8688	18	US-10-622-088-105	Sequence 105, App
45	21.6	86.4	9249	15	US-10-389-120-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-732-914-12  
; Sequence 12, Application US/09732914  
; Patent No. US20020007051A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheo, David  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Hartley, James L.  
; APPLICANT: Byrd, Devon R.N.  
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in  
; FILE REFERENCE: 0942.5010002  
; CURRENT APPLICATION NUMBER: US/09/732.914  
; CURRENT FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 60/169,983  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: US 60/188,020  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: attR2  
US-09-732-914-12

Query Match 86.4%; Score 21.6; DB 9; Length 25;  
Best Local Similarity 76.0%; Pred. No. 1.4; Indels 0; Gaps 0;  
Matches 19; Conservative 5; Mismatches 1;  
Oy 1 GTTCAGCTTTTCTTACNAAGTSGB 25  
Db 1 GTTCAGCTTTTCTTACNAAGTGGT 25

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RESULT 2
US-09-855-797A-5
; Sequence 5, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-5

Query Match      86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKTRTACNAAGTSGB 25
Db 1 GTTCAGCTTTTKTRTACNAAGTSGB 25

RESULT 3
US-09-855-797A-11
; Sequence 11, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-11

Query Match      86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.4;
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Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKTRTACNAAGTSGB 25
Db 1 GTTCAGCTTTCTGTACAAAGTGGT 25

RESULT 4
US-09-907-900-5
; Sequence 5, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-5

Query Match      86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKTRTACNAAGTSGB 25
Db 1 GTTCAGCTTTTKTRTACNAAGTSGB 25

RESULT 5
US-09-907-900-11
; Sequence 11, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-11
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Query Match 86.4%; Score 21.6; DB 9; Length 25;  
Best Local Similarity 76.0%; Pred. No. 1.4;  
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKTRTACNAAGTSG 25  
|||||:|||||:|||||:|||||:  
Db 1 GTTCAGCTTTCTGTACAAAGTGGT 25

## RESULT 6

US-09-907-719-5  
; Sequence 5, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: 18  
; OTHER INFORMATION: "n" may be any nucleotide  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-719-5

Query Match 86.4%; Score 21.6; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKTRTACNAAGTSG 25  
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Db 1 GTTCAGCTTTTKTRTACNAAGTSG 25

## RESULT 7

US-09-907-719-11  
; Sequence 11, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products

## US-09-907-719-11

Query Match 86.4%; Score 21.6; DB 9; Length 25;  
Best Local Similarity 76.0%; Pred. No. 1.4;  
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKTRTACNAAGTSG 25  
|||||:|||||:|||||:|||||:  
Db 1 GTTCAGCTTTCTGTACAAAGTGGT 25

## RESULT 8

US-09-432-085-5  
; Sequence 5, Application US/09432085  
; Publication No. US20030100110A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,085  
; FILING DATE: (Herewith)  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
US-09-432-085-5

Query Match 86.4%; Score 21.6; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKTRTACNAAGTSG 25  
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Db 1 GTTCAGCTTTTKTRTACNAAGTSG 25

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RESULT 9
US-09-985-448-5
; Sequence 5, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-5

Query Match      86.4%; Score 21.6; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTXYKTRTACNAAGTSG 25
Db 1 GTTCAGCTTTTXYKTRTACNAAGTSG 25

RESULT 10
US-09-985-448-11
; Sequence 11, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-11

Query Match      86.4%; Score 21.6; DB 10; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTXYKTRTACNAAGTSG 25
Db 1 GTTCAGCTTTTXYKTRTACNAAGTSG 25
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Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTXYKTRTACNAAGTSG 25
Db 1 GTTCAGCTTTTCTGTGACAAAGTGGT 25

RESULT 11
US-10-058-292-5
; Sequence 5, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-058-292-5

Query Match      86.4%; Score 21.6; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTXYKTRTACNAAGTSG 25
Db 1 GTTCAGCTTTTXYKTRTACNAAGTSG 25

RESULT 12
US-10-058-291-5
; Sequence 5, Application US/10058291
; Publication No. US20030064515A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
```



;; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
;; Recombination Sites  
;; NUMBER OF SEQUENCES: 35  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
;; STREET: 1100 New York Ave., N. W. Suite 600  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005-3934  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/058,291  
;; FILING DATE: 30-Jan-2002  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/432,085  
;; FILING DATE: 1999-11-02  
;; APPLICATION NUMBER: 09/233,493  
;; FILING DATE: 20-JAN-1999  
;; APPLICATION NUMBER: 09/005,476  
;; FILING DATE: 12-JAN-1998  
;; APPLICATION NUMBER: 08/663,002  
;; FILING DATE: 07-JUN-1996  
;; APPLICATION NUMBER: 08/486,139  
;; FILING DATE: 07-JUN-1995  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2540  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-058-291-5  
Query Match 86.4%; Score 21.6; DB 14; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTTCAGCTTTTKRTACNAAGTSG 25  
Db 1 GTTCAGCTTTTKRTACNAAGTSG 25  
RESULT 13  
US-10-162-879-5  
; Sequence 5, Application US/10162879  
; Publication No. US20030068799A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Bransch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/162,879  
;; FILING DATE: 06-Jun-2002  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/432,085  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: 09/233,493  
;; FILING DATE: 20-JAN-1999  
;; APPLICATION NUMBER: 09/005,476  
;; FILING DATE: 12-JAN-1998  
;; APPLICATION NUMBER: 08/663,002  
;; FILING DATE: 07-JUN-1996  
;; APPLICATION NUMBER: 08/486,139  
;; FILING DATE: 07-JUN-1995  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; MOLECULE TYPE: cDNA  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-162-879-5  
Query Match 86.4%; Score 21.6; DB 14; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTTCAGCTTTTKRTACNAAGTSG 25  
Db 1 GTTCAGCTTTTKRTACNAAGTSG 25  
RESULT 14  
US-10-161-403-45  
; Sequence 45, Application US/10161403  
; Publication No. US20030119104A1  
; GENERAL INFORMATION:  
; APPLICANT: Perkins, Edward  
; APPLICANT: Perez, Carl  
; APPLICANT: Lindenbaum, Michael  
; APPLICANT: Greene, Amy  
; APPLICANT: Leung, Josephine  
; APPLICANT: Fleming, Elena  
; APPLICANT: Stewart, Sandra  
; APPLICANT: Shellard, Joan  
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS  
; FILE REFERENCE: 24601-420  
; CURRENT APPLICATION NUMBER: US/10/161,403  
; CURRENT FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/294,758  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: 60/366,891  
; PRIOR FILING DATE: 2002-03-21  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: m-attP1  
; FEATURE:  
; NAME/KEY: misc\_difference  
; LOCATION: 18  
; OTHER INFORMATION: n is a or g or c or t/u  
US-10-161-403-45

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Query Match      86.4%; Score 21.6; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTKYKRTACNAAGTSGB 25
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Db 1 GTTCAGCTTTKYKRTACNAAGTSGB 25

RESULT 15
US-10-151-690-36
; Sequence 36, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr2
US-10-151-690-36

Query Match      86.4%; Score 21.6; DB 15; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.4;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTKYKRTACNAAGTSGB 25
   |||||
Db 1 GTTCAGCTTTCTGTACAAAGTGGT 25

Search completed: November 16, 2004, 11:14:59
Job time : 314.1 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds  
(without alignments)  
594.643 Million cell updates/sec

Title: US-10-820-133-5

Perfect score: 25

Sequence: 1 gttcagcttcttctacnaagtsb 25

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gse1:\*

9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	21.6	86.4	753	8 AQ990861	AQ990861 Rfc01698
C 3	21.6	86.4	808	8 AQ990388	AQ990388 Rfc01153
C 4	20.6	82.4	719	8 AQ991352	AQ991352 Rfc02270
C 5	20.4	81.6	206	5 B0156416	B0156416 NF092F021
C 6	20.4	81.6	299	5 B115594	B115594 BY115594
C 7	20.4	81.6	306	5 B0156416	B0156416 NF092F021
C 8	20.4	81.6	374	5 B0156416	B0156416 NF092F021
C 9	20.4	81.6	401	5 B0156416	B0156416 NF092F021
C 10	20.4	81.6	409	5 B0156416	B0156416 NF092F021
C 11	20.4	81.6	422	5 B0156416	B0156416 NF092F021
C 12	20.4	81.6	423	5 B0156416	B0156416 NF092F021
C 13	20.4	81.6	430	5 B0156416	B0156416 NF092F021
C 14	20.4	81.6	432	5 B0156416	B0156416 NF092F021
C 15	20.4	81.6	443	5 B0156416	B0156416 NF092F021
C 16	20.4	81.6	443	5 B0156416	B0156416 NF092F021
C 17	20.4	81.6	449	5 B0156416	B0156416 NF092F021
C 18	20.4	81.6	472	5 B0156416	B0156416 NF092F021
C 19	20.4	81.6	473	5 B0156416	B0156416 NF092F021
C 20	20.4	81.6	482	5 B0156416	B0156416 NF092F021
C 21	20.4	81.6	483	5 B0156416	B0156416 NF092F021
C 22	20.4	81.6	486	5 B0156416	B0156416 NF092F021
C 23	20.4	81.6	489	5 B0156416	B0156416 NF092F021
C 24	20.4	81.6	546	5 B0156416	B0156416 NF092F021

C 25	20.4	81.6	567	5 BP754491	BP754491 BP754491
C 26	20.4	81.6	597	4 B1422679	B1422679 EST533345
C 27	20.4	81.6	645	5 BP754484	BP754484 BP754484
C 28	20.4	81.6	671	5 BP754388	BP754388 BP754388
C 29	20.4	81.6	672	5 BP754535	BP754535 BP754535
C 30	20.4	81.6	674	5 BP754519	BP754519 BP754519
C 31	20.4	81.6	689	5 BP754572	BP754572 BP754572
C 32	20.4	81.6	695	8 AQ991039	AQ991039 Rfc01894
C 33	20.4	81.6	712	8 AQ990809	AQ990809 Rfc01638
C 34	20.4	81.6	731	5 BP758121	BP758121 BP758121
C 35	20.4	81.6	743	8 AQ990346	AQ990346 Rfc01106
C 36	20.4	81.6	764	8 AQ990110	AQ990110 Rfc00827
C 37	20.4	81.6	769	8 AQ990470	AQ990470 Rfc01245
C 38	20.0	80.0	321	2 BF086649	BF086649 CMO-GN007
C 39	20.0	80.0	595	2 AW993039	AW993039 KC2-BN003
C 40	20.0	80.0	635	7 CN484020	CN484020 hw41b03.Y
C 41	20.0	80.0	675	8 AQ991241	AQ991241 Rfc02132
C 42	20.0	80.0	706	4 B1836912	B1836912 603084230
C 43	20.0	80.0	714	5 BX359053	BX359053 BX359053
C 44	20.0	80.0	752	4 BG620766	BG620766 602617479
C 45	20.0	80.0	797	4 BG427603	BG427603 602497040

## ALIGNMENTS

RESULT 1  
AQ990864/c

LOCUS  
AQ990864 672 bp DNA linear GSS 14-AUG-2000

DEFINITION  
Rfc01701 Photorhabdus luminescens strain W14 M13 library  
Photorhabdus luminescens genomic clone PLG01701, genomic survey sequence.

ACCESSION  
AQ990864

VERSION  
AQ990864.1 GI:9649458

KEYWORDS  
GSS.

SOURCE  
Photorhabdus luminescens

ORGANISM  
Photorhabdus luminescens

REFERENCE  
1 (bases 1 to 672)  
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.  
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL  
MEDLINE  
20378633

PUBMED  
10919786

COMMENT  
Contact: ffrench-Constant RH  
Department of Biology and Biochemistry  
University of Bath  
South Building, Bath BA2 7AY, UK  
Tel: (44) 1225 826621  
Fax: (44) 1225 826779  
Email: bsarfc@bath.ac.uk  
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.  
Seq primer: M13 Forward  
Class: shotgun.  
Location/Qualifiers  
1. .672  
/organism="Photorhabdus luminescens"  
/mol\_type="genomic DNA"  
/strain="W14"  
/db\_xref="taxon:29488"  
/clones="PLG01701"  
/dev\_stage="primary phase variant"  
/clone\_lib="Photorhabdus luminescens strain W14 M13 library"  
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 86.4%; Score 21.6; DB 8; Length 672;  
 Best Local Similarity 76.0%; Pred. No. 19;  
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25  
 |||||:||||:||||:||||:||||:  
 Db 637 GTTCAGCTTTTATATAAGTGGC 613

RESULT 2  
 AQ90861/c  
 LOCUS  
 DEFINITION Rfc01698 Photorhabdus luminescens strain W14 M13 library  
 Photorhabdus luminescens genomic clone PLG01698, genomic survey  
 sequence.

ACCESSION AQ90861  
 VERSION AQ90861.1 GI:9649455  
 KEYWORDS GSS.  
 SOURCE Photorhabdus luminescens  
 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 753)  
 AUTHORS fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,  
 Daborn,P.J., Bowen,D. and Blattner,F.R.  
 TITLE A genomic sample sequence of the entomopathogenic bacterium  
 Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)  
 MEDLINE 20378633  
 PUBMED 10919786

COMMENT Contact: fFrench-Constant RH  
 Department of Biology and Biochemistry  
 University of Bath  
 South Building, Bath BA2 7AY, UK  
 Tel: (44) 1225 826621  
 Fax: (44) 1225 826779  
 Email: bssrfc@bath.ac.uk  
 This is one of 2,122 random reads from the M13 library. For  
 annotation of identified clones (BLASTX, BLASTN and mapping to E.  
 coli K12 genome) please see fFrench-Constant et al. 2000, Nucleic  
 Acids Res.

Seq primer: M13 Forward  
 Class: shotgun.

FEATURES  
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 Location/Qualifiers  
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 /db\_xref="taxon:29488"  
 /clone="PLG01698"  
 /dev\_stage="primary phase variant"  
 /clone\_lib="Photorhabdus luminescens strain W14 M13  
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 /note="Genomic DNA from strain W14 was size selected (1-2  
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Query Match 86.4%; Score 21.6; DB 8; Length 753;  
 Best Local Similarity 76.0%; Pred. No. 19;  
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25  
 |||||:||||:||||:||||:||||:  
 Db 638 GTTCAGCTTTTATATAAGTGGC 614

RESULT 3  
 AQ90861/c  
 LOCUS  
 DEFINITION Rfc01698 Photorhabdus luminescens strain W14 M13 library  
 Photorhabdus luminescens genomic clone PLG01698, genomic survey  
 sequence.

ACCESSION AQ90861  
 VERSION AQ90861.1 GI:9649455  
 KEYWORDS GSS.  
 SOURCE Photorhabdus luminescens  
 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 753)  
 AUTHORS fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,  
 Daborn,P.J., Bowen,D. and Blattner,F.R.  
 TITLE A genomic sample sequence of the entomopathogenic bacterium  
 Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)  
 MEDLINE 20378633  
 PUBMED 10919786

COMMENT Contact: fFrench-Constant RH  
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 Fax: (44) 1225 826779  
 Email: bssrfc@bath.ac.uk  
 This is one of 2,122 random reads from the M13 library. For  
 annotation of identified clones (BLASTX, BLASTN and mapping to E.  
 coli K12 genome) please see fFrench-Constant et al. 2000, Nucleic  
 Acids Res.

Seq primer: M13 Forward  
 Class: shotgun.

ACCESSION AQ990388  
 VERSION AQ990388.1 GI:9648982  
 KEYWORDS GSS.  
 SOURCE Photorhabdus luminescens  
 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 808)  
 AUTHORS fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,  
 Daborn,P.J., Bowen,D. and Blattner,F.R.  
 TITLE A genomic sample sequence of the entomopathogenic bacterium  
 Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)  
 MEDLINE 20378633  
 PUBMED 10919786

COMMENT Contact: fFrench-Constant RH  
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 University of Bath  
 South Building, Bath BA2 7AY, UK  
 Tel: (44) 1225 826621  
 Fax: (44) 1225 826779  
 Email: bssrfc@bath.ac.uk  
 This is one of 2,122 random reads from the M13 library. For  
 annotation of identified clones (BLASTX, BLASTN and mapping to E.  
 coli K12 genome) please see fFrench-Constant et al. 2000, Nucleic  
 Acids Res.

Seq primer: M13 Forward  
 Class: shotgun.

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 Location/Qualifiers  
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 /dev\_stage="primary phase variant"  
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 /note="Genomic DNA from strain W14 was size selected (1-2  
 kb) and then cloned into M13 Janus."

Query Match 86.4%; Score 21.6; DB 8; Length 808;  
 Best Local Similarity 76.0%; Pred. No. 19;  
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25  
 |||||:||||:||||:||||:||||:  
 Db 628 GTTCAGCTTTTATATAAGTGGC 604

RESULT 4  
 AQ991352/c  
 LOCUS  
 DEFINITION Rfc02270 Photorhabdus luminescens strain W14 M13 library  
 Photorhabdus luminescens genomic clone PLG02270, genomic survey  
 sequence.

ACCESSION AQ991352  
 VERSION AQ991352.1 GI:9649946  
 KEYWORDS GSS.  
 SOURCE Photorhabdus luminescens  
 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 719)  
 AUTHORS fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,  
 Daborn,P.J., Bowen,D. and Blattner,F.R.  
 TITLE A genomic sample sequence of the entomopathogenic bacterium  
 Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)  
 MEDLINE 20378633  
 PUBMED 10919786

COMMENT Contact: fFrench-Constant RH  
 Department of Biology and Biochemistry  
 University of Bath  
 South Building, Bath BA2 7AY, UK  
 Tel: (44) 1225 826621  
 Fax: (44) 1225 826779  
 Email: bssrfc@bath.ac.uk  
 This is one of 2,122 random reads from the M13 library. For  
 annotation of identified clones (BLASTX, BLASTN and mapping to E.  
 coli K12 genome) please see fFrench-Constant et al. 2000, Nucleic  
 Acids Res.

Seq primer: M13 Forward  
 Class: shotgun.

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Fax: (44) 1225 826779  
Email: bsarf@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For  
annotation of identified clones (BLASTX, BLASTN and mapping to E.  
coli K12 genome) please see firench-Constant et al. 2000, Nucleic  
Acids Res.

Seq primer: M13 Forward

Class: shotgun.

Location/Qualifiers

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FEATURES  
source

#### ORIGIN

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Best Local Similarity 72.0%; Pred. No. 57;  
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GTTCAGCTTTTKTRTACNAAGTSGB 25  
|||||:|||||:|||||:|||||:  
Db 638 GTTCAGCTTTTATANTAGTGGC 614

#### RESULT 5

BQ156416/c  
LOCUS BQ156416 206 bp mRNA linear EST 24-APR-2002  
DEFINITION NF092F02IR1F1027 Irradiated Medicago truncatula cDNA clone  
NF092F02IR 5', mRNA sequence.  
ACCESSION BQ156416  
VERSION BQ156416  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
REFERENCE 1 (bases 1 to 206)  
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula irradiated library  
Unpublished (2001)  
CONTACT: May GD  
PLANT Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 224 6650  
Fax: 580 224 6692  
Email: gdmay@noble.org  
Insert Length: 206 Std Error: 0.00  
Plate: 092 row: F column: 02  
Seq primer: TCACACAGAACACTATGAC.

Location/Qualifiers

1..206  
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/dev\_stage="seedling"

FEATURES  
source

/clone\_lib="Irradiated"  
/note="Vector: Lambda Zap; Seedlings were exposed either  
to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.  
Gamma-irradiated samples were harvested at 6, 12, 24 and  
48 hours after treatment. UV-irradiated samples were  
harvested 24 hours post-treatment. cDNA was prepared from  
polyA+ enriched, pooled samples of equivalent amounts of  
total RNA from each sample. The cDNA was directionally  
ligated into the Uni-Zap XR vector (Stratagene) and  
packaged using the Gigapack III Gold packaging extracts.  
Phagemids containing cDNA inserts were in vivo excised  
from the recombinant Uni-Zap XR vector using ExAssist  
helper phage and the E. coli strain XL1-Blue MRF'  
(Stratagene). Excised plasmids were plated using SOLR  
cells."

#### ORIGIN

Query Match 81.6%; Score 20.4; DB 5; Length 206;  
Best Local Similarity 76.0%; Pred. No. 60;  
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GTTCAGCTTTTKTRTACNAAGTSGB 25  
|||||:|||||:|||||:|||||:  
Db 167 GTTCAGCTTTTATACTAAGTGG 143

#### RESULT 6

BY115594  
LOCUS BY115594 299 bp mRNA linear EST 08-DEC-2002  
DEFINITION BY115594 RIKEN full-length enriched, 18 days embryo whole body Mus  
musculus cDNA clone L430040C03 5', mRNA sequence.  
ACCESSION BY115594  
VERSION BY115594.1 GI:26226695  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 299)  
Okazaki,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,  
Nikaido,I., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,  
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,  
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,  
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,  
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,  
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,  
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,  
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,  
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,  
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konegaya,A.,  
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,  
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,  
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,  
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,  
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,  
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,  
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,  
Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,  
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,  
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,  
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,  
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,  
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,  
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,  
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,  
Rogers,J., Birney,E. and Hayashizaki,Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

#### TITLE

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Yoshihide Hayashizaki

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Sciences Center(GSC), Yokohama Institute  
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 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Aikawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,  
 Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,  
 Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,  
 Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,  
 Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and  
 Hayashizaki,Y. Direct Submission  
 Computational Analysis of Full-length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.

## FEATURES

source  
 location/Qualifiers  
 1. .299  
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 /dev\_stage="18 days embryo"  
 /clone\_lib="RIKEN full-length enriched, 18 days embryo  
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## ORIGIN

Query Match 81.6%; Score 20.4; DB 5; Length 299;  
 Best Local Similarity 76.0%; Pred. No. 63;  
 Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSG 25

Db 246 GTTCAGCTTTTATACAAAGTTGG 270

RESULT 7  
 BP757615/c 306 bp mRNA linear EST 08-JUL-2004  
 LOCUS  
 DEFINITION BP757615 mouse (C57BL/6) pancreatic islet library with  
 recombination-based method Mus musculus cDNA clone mib04031 3',  
 mRNA sequence.

VERSION BP757615.1 GI:50077505

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 306)

TITLE Takeda,J., Ohara,O. and Seino,S.  
 Construction of a multi-functional cDNA library specific for mouse  
 pancreatic islets and its application to microarray

JOURNAL Unpublished (2004)

COMMENT Contact: Susumu Seino

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 Email: seino@med.kobe-u.ac.jp.

Kobe University Graduate School of Medicine  
 7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan  
 Tel: 81-78-382-5360  
 Fax: 81-78-382-5370  
 Email: seino@med.kobe-u.ac.jp.

## FEATURES

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 recombination-based method"

## ORIGIN

Query Match 81.6%; Score 20.4; DB 5; Length 306;  
 Best Local Similarity 76.0%; Pred. No. 64;  
 Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSG 25

Db 109 GTTCAGCTTTTGTACAAAGTTGG 85

## RESULT 8

BP754432/c

LOCUS

DEFINITION

BP754432 mouse (C57BL/6) pancreatic islet library with  
 recombination-based method Mus musculus cDNA clone mib0061 3',  
 mRNA sequence.

ACCESSION BP754432

VERSION BP754432.1 GI:50074322

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 374)

Takeda,J., Ohara,O. and Seino,S.

Construction of a multi-functional cDNA library specific for mouse

pancreatic islets and its application to microarray

Unpublished (2004)

JOURNAL

COMMENT Contact: Susumu Seino

Division of Cellular and Molecular Medicine

Kobe University Graduate School of Medicine

7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan

Tel: 81-78-382-5360

Fax: 81-78-382-5370

Email: seino@med.kobe-u.ac.jp.

## FEATURES

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 location/Qualifiers  
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 /mol\_type="mRNA"  
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 /sex="male"  
 /tissue\_type="pancreatic islet"  
 /dev\_stage="adult"  
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 recombination-based method"

## ORIGIN

Query Match 81.6%; Score 20.4; DB 5; Length 374;

Best Local Similarity 76.0%; Pred. No. 65;

Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSG 25

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73 GTTCAGCTTTTGTACAAAGTTGG 49

Db
RESULT 9
BP754410/c
LOCUS
DEFINITION BP754410 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial0045 3',
mRNA sequence.
ACCESSION BP754410
VERSION BP754410.1 GI:50074300
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 401)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
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FEATURES
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recombination-based method"

ORIGIN
Query Match 81.6%; Score 20.4; DB 5; Length 401;
Best Local Similarity 76.0%; Pred. No. 66;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTSCB 25
|||||
Db 52 GTTCAGCTTTTGTACAAAGTTGG 28

RESULT 11
BP754464/c
LOCUS
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recombination-based method Mus musculus cDNA clone mial0085 3',
mRNA sequence.
ACCESSION BP754464
VERSION BP754464.1 GI:50074354
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 422)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
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Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
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recombination-based method"

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Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTSCB 25
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Db 52 GTTCAGCTTTTGTACAAAGTTGG 28

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recombination-based method Mus musculus cDNA clone mial1051 3',
mRNA sequence.
ACCESSION BP754552
VERSION BP754552.1 GI:50074442
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 409)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino

```

```

Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
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Best Local Similarity 76.0%; Pred. No. 66;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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mRNA sequence.
ACCESSION BP754464
VERSION BP754464.1 GI:50074354
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 422)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
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Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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RESULT 10
BP754552/c
LOCUS
DEFINITION BP754552 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial1051 3',
mRNA sequence.
ACCESSION BP754552
VERSION BP754552.1 GI:50074442
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 409)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino

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Qy 1 GTTCAGCTTTTKRTACNAAGTSG 25  
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Db 73 GTTCAGCTTTTGTACAAAGTTGG 49

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recombination-based method Mus musculus cDNA clone mial1021 3',  
mRNA sequence.  
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BP754508.1 GI:50074398  
EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
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1. (bases 1 to 443)  
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,  
Takeda,J., Ohara,O. and Seino,S.  
TITLE Construction of a multi-functional cDNA library specific for mouse  
pancreatic islets and its application to microarray  
JOURNAL Unpublished (2004)  
COMMENT Contact: Sueumu Seino  
Division of Cellular and Molecular Medicine  
Kobe University Graduate School of Medicine  
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan  
Tel: 81-78-382-5360  
Fax: 81-78-382-5370  
Email: seino@med.kobe-u.ac.jp.

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Job time : 1534 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:43 ; Search time 708.5 Seconds  
(without alignments)  
1668.656 Million cell updates/sec

Title: US-10-820-133-39  
Perfect score: 25  
Sequence: 1 rbycwgctttrttacwaaastkgd 25

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Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	20.2	80.8	25	6	AR124530 Sequence
6	20.2	80.8	25	6	AR124531 Sequence
7	20.2	80.8	25	6	AR124532 Sequence
8	20.2	80.8	25	6	AR124533 Sequence
9	20.2	80.8	25	6	AR124534 Sequence
10	20.2	80.8	25	6	AR124535 Sequence
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17	20.2	80.8	25	6	AR124542 Sequence
18	20.2	80.8	25	6	AR124543 Sequence
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c 31	20.2	80.8	25	6	AR163205 Sequence
c 32	20.2	80.8	25	6	AR163206 Sequence
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DEFINITION AR124526  
ACCESSION AR124526  
VERSION AR124526.1 GI:14109887  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: US 6171861-A 6 09-JAN-2001;  
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ACCESSION	AR124527	
VERSION	AR124527.1 GI:14109888	
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 25)	
AUTHORS	Hartley,J.L. and Brasch,M.A.	
TITLE	Recombinational cloning using engineered recombination sites	

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DEFINITION Sequence 8 from patent US 6171861.
ACCESSION AR124528
VERSION AR124528.1 GI:14109889
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 8 09-JAN-2001;
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DEFINITION Sequence 9 from patent US 6171861.
ACCESSION AR124529
VERSION AR124529.1 GI:14109890
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 9 09-JAN-2001;
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DEFINITION Sequence 10 from patent US 6171861.
ACCESSION AR124530
VERSION AR124530.1 GI:14109891
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
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ACCESSION AR124531
VERSION AR124531.1 GI:14109892
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 11 09-JAN-2001;
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DEFINITION Sequence 12 from patent US 6171861.
ACCESSION AR124532
VERSION AR124532.1 GI:14109893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 12 09-JAN-2001;
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-10-820-133-39  
Perfect score: 25  
Sequence: 1 rbycwgcttctttrtaacaaastkgd 25

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Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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13	20.2	80.8	25	2	AAT48214
14	20.2	80.8	25	2	AAT48213
15	20.2	80.8	25	2	AAT48212
16	20.2	80.8	25	2	AAT48211
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21	20.2	80.8	25	2	AAT48206

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27	20.2	80.8	25	2	AAX78949
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## ALIGNMENTS

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XX AAT48216;

DT 20-OCT-1997 (first entry)

XX attB2 core region.

XX att recombination site; core region; mutation; enhance; recombination;  
vector; subcloning; regulation; exchange; ss.

OS Synthetic.

XX WO9640724-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US010082.

XX 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;

XX WPI, 1997-065168/06.

PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
using recombinant proteins and engineered recombination sites in vitro or  
in vivo.

XX Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The  
core region has at least one engineered mutation that enhances  
recombination in vitro in the formation of a Co-integrate or Product DNA.  
These core regions can be incorporated into novel vector donor DNA  
molecules. The nucleic acids, vectors and methods of the invention are  
used to obtain chimeric nucleic acid using recombination proteins and  
engineered recombination sites in vitro or in vivo. The improved  
specificity, speed and yields of the invention facilitates DNA or RNA  
subcloning, regulation or exchange useful for any related purpose, e.g.

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CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA
XX
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Query Match      80.8%; Score 20.2; DB 2; Length 25;
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DT 20-OCT-1997 (first entry)
XX
DE attP2, P3 core region.
XX
KW att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
XX
OS Synthetic.
XX
PN WO9640724-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010082.
XX
PR 07-JUN-1995; 95US-00486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA;
XX
DR WPI; 1997-065168/06.
XX
PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in vitro or
PT in vivo.
XX
PS Claim 14; Page 56; 106pp; English.
XX
CC AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA
XX
SQ Sequence 25 BP; 5 A; 6 C; 4 G; 10 T; 0 U; 0 Other;

Query Match      80.8%; Score 20.2; DB 2; Length 25;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCWGCTTTTTRTACWAASTKGD 25
   ::::::::::::::::::::
Db 1 GTTCAGCTTCTGTACAAACTGG 25

RESULT 3
AAT48215
ID AAT48215 standard; DNA; 25 BP.
XX
AC AAT48215;
XX
DT 20-OCT-1997 (first entry)
XX
DE attB1 core region.
XX
KW att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
XX
OS Synthetic.
XX
PN WO9640724-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010082.
XX
PR 07-JUN-1995; 95US-00486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA;
XX
DR WPI; 1997-065168/06.
XX
PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in vitro or
PT in vivo.
XX
PS Claim 14; Page 55; 106pp; English.
XX
CC AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA
XX
SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

Query Match      80.8%; Score 20.2; DB 2; Length 25;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCWGCTTTTTRTACWAASTKGD 25
   ::::::::::::::::::::
Db 1 AGCCTGCTTCTGTACAAACTGT 25

RESULT 4
AAT48221
ID AAT48221 standard; DNA; 25 BP.
XX
AC AAT48221;
XX
DT 20-OCT-1997 (first entry)
XX
DE attL1 core region.
XX
KW att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
XX
```





CC engineered recombination sites in vitro or in vivo. The improved  
 CC specificity, speed and yields of the invention facilitates DNA or RNA  
 CC subcloning, regulation or exchange useful for any related purpose, e.g.  
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA

SQ Sequence 25 BP; 5 A; 5 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 2; Length 25;  
 Best Local Similarity 60.0%; Pred. No. 28;  
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCWGCTTTTTRTACWAASTKGD 25

Db 1 AGCGTGCTTTCTTGTCACAAAGTTGG 25

# RESULT 7

AAT48223

ID AAT48223 standard; DNA; 25 BP.

XX AC AAT48223;

DT 20-OCT-1997 (first entry)

XX DE attL3 core region.

XX att recombination site; core region; mutation; enhance; recombination;  
 KW vector; subcloning; regulation; exchange; ss.

XX Synthetic.

XX WO9640724-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;

XX DR WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
 PT using recombinant proteins and engineered recombination sites in vitro or  
 PT in vivo.

PS Claim 14; Page 56; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The  
 CC core region has at least one engineered mutation that enhances  
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.  
 CC These core regions can be incorporated into novel vector donor DNA  
 CC molecules. The nucleic acids, vectors and methods of the invention are  
 CC used to obtain chimeric nucleic acid using recombination proteins and  
 CC engineered recombination sites in vitro or in vivo. The improved  
 CC specificity, speed and yields of the invention facilitates DNA or RNA  
 CC subcloning, regulation or exchange useful for any related purpose, e.g.  
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA

SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 2; Length 25;  
 Best Local Similarity 60.0%; Pred. No. 28;  
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCWGCTTTTTRTACWAASTKGD 25

Db 1 ACCCAGCTTTCTTGTCACAAAGTTGG 25

# RESULT 8

AAT48224

ID AAT48224 standard; DNA; 25 BP.

XX AC AAT48224;

DT 20-OCT-1997 (first entry)

XX DE attP1 core region.

XX att recombination site; core region; mutation; enhance; recombination;  
 KW vector; subcloning; regulation; exchange; ss.

XX Synthetic.

XX WO9640724-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;

XX DR WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
 PT using recombinant proteins and engineered recombination sites in vitro or  
 PT in vivo.

PS Claim 14; Page 56; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The  
 CC core region has at least one engineered mutation that enhances  
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.  
 CC These core regions can be incorporated into novel vector donor DNA  
 CC molecules. The nucleic acids, vectors and methods of the invention are  
 CC used to obtain chimeric nucleic acid using recombination proteins and  
 CC engineered recombination sites in vitro or in vivo. The improved  
 CC specificity, speed and yields of the invention facilitates DNA or RNA  
 CC subcloning, regulation or exchange useful for any related purpose, e.g.  
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA

SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 2; Length 25;  
 Best Local Similarity 60.0%; Pred. No. 28;  
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCWGCTTTTTRTACWAASTKGD 25

Db 1 GTTCAGCTTTTTRTGTACAAAGTTGG 25

# RESULT 9

AAT48218

ID AAT48218 standard; DNA; 25 BP.

XX AC AAT48218;

DT 20-OCT-1997 (first entry)

XX DE attR1 core region.

KW att recombination site; core region; mutation; enhance; recombination;  
 XX vector; subcloning; regulation; exchange; ss.  
 OS Synthetic.  
 XX WO9640724-A1.  
 PN 19-DEC-1996.  
 PD  
 XX 07-JUN-1996; 96WO-US010082.  
 XX 07-JUN-1995; 95US-00486139.  
 XX (LIFE-) LIFE TECHNOLOGIES INC.  
 XX Hartley JL, Brasch MA;  
 XX WPI; 1997-065168/06.  
 XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
 PT using recombinant proteins and engineered recombination sites in vitro or  
 PT in vivo.  
 XX Claim 14; Page 55; 106pp; English.  
 XX AAT48210-25 are att recombination site core region DNA sequences. The  
 CC core region has at least one engineered mutation that enhances  
 CC recombination in vitro in the formation of a Co-integrate or Product DNA.  
 CC These core regions can be incorporated into novel vector donor DNA  
 CC molecules. The nucleic acids, vectors and methods of the invention are  
 CC used to obtain chimeric nucleic acid using recombination proteins and  
 CC engineered recombination sites in vitro or in vivo. The improved  
 CC specificity, speed and yields of the invention facilitates DNA or RNA  
 CC subcloning, regulation or exchange useful for any related purpose, e.g.  
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA  
 XX  
 XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;  
 SQ  
 Query Match 80.8%; Score 20.2; DB 2; Length 25;  
 Best Local Similarity 60.0%; Pred. No. 28;  
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RBVCWGCTTTTTRTACWAASTKGD 25  
 :::::|||||:|||||:|||||:|:  
 Db 1 GTTCAGCTTTTGTACAACTTGT 25  
 RESULT 10  
 AAT48217  
 ID AAT48217 standard; DNA; 25 BP.  
 XX  
 AC AAT48217;  
 XX  
 XX 20-OCT-1997 (first entry)  
 DT  
 XX attB3 core region.  
 DE  
 XX att recombination site; core region; mutation; enhance; recombination;  
 KW vector; subcloning; regulation; exchange; ss.  
 XX Synthetic.  
 XX WO9640724-A1.  
 XX 19-DEC-1996.  
 XX 07-JUN-1996; 96WO-US010082.  
 XX 07-JUN-1995; 95US-00486139.  
 XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;  
 XX WPI; 1997-065168/06.  
 XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
 PT using recombinant proteins and engineered recombination sites in vitro or  
 PT in vivo.  
 XX Claim 14; Page 55; 106pp; English.  
 XX AAT48210-25 are att recombination site core region DNA sequences. The  
 CC core region has at least one engineered mutation that enhances  
 CC recombination in vitro in the formation of a Co-integrate or Product DNA.  
 CC These core regions can be incorporated into novel vector donor DNA  
 CC molecules. The nucleic acids, vectors and methods of the invention are  
 CC used to obtain chimeric nucleic acid using recombination proteins and  
 CC engineered recombination sites in vitro or in vivo. The improved  
 CC specificity, speed and yields of the invention facilitates DNA or RNA  
 CC subcloning, regulation or exchange useful for any related purpose, e.g.  
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA  
 XX  
 XX Sequence 25 BP; 6 A; 7 C; 3 G; 9 T; 0 U; 0 Other;  
 SQ  
 Query Match 80.8%; Score 20.2; DB 2; Length 25;  
 Best Local Similarity 60.0%; Pred. No. 28;  
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RBVCWGCTTTTTRTACWAASTKGD 25  
 :::::|||||:|||||:|||||:|:  
 Db 1 ACCCAGCTTTTGTACAACTTGT 25  
 RESULT 11  
 AAX78973  
 ID AAX78973 standard; DNA; 25 BP.  
 XX  
 AC AAX78973;  
 XX  
 XX 17-AUG-1999 (first entry)  
 DT  
 XX Oligonucleotide #39 for recombination and cloning method.  
 DE  
 XX Cloning; donor; recombination site; vector; chimeric; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9921977-A1.  
 PN  
 XX 06-MAY-1999.  
 PD  
 XX 26-OCT-1998; 98WO-US022589.  
 XX  
 XX 24-OCT-1997; 97US-0065930P.  
 PR  
 XX 23-OCT-1998; 98US-00177387.  
 PR  
 XX (LIFE-) LIFE TECHNOLOGIES INC.  
 PA  
 XX Hartley JL, Brasch MA, Temple GF, Fox DK;  
 PI  
 XX WPI; 1999-303011/25.  
 XX  
 XX New nucleic acid cloning methods.  
 PT  
 XX Disclosure; Page 169; 185pp; English.  
 PS  
 XX The invention relates to novel methods for cloning or subcloning one or  
 CC more nucleic acid molecules (NAs) comprising: (a) combining in vitro or  
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
 CC more desired nucleic acid segments flanked by at least 2 recombination  
 CC sites which do not recombine with each other; (2) one or more vector

CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
CC not recombine with each other; and (3) one or more site-specific  
CC recombination proteins; (b) incubating the combination to transfer one or  
CC more of the desired segments into one or more of the VDMs, thereby  
CC producing one or more desired product molecules (PMS). The methods can be  
CC used for the efficient and specific recombination of NAM segments. They  
CC can be used to generate chimeric DNA or RNA molecules that have the  
CC desired characteristics and/or nucleic acid segments. The methods can  
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
CC are used in the method of the invention

XX Sequence 25 BP; 3 A; 3 C; 2 G; 7 T; 0 U; 10 Other;

Query Match 80.8%; Score 20.2; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
Db 1 RBYCWGCTTTTTRTACWAASTKGD 25

## RESULT 12

AAX78994  
ID AAX78994 standard; DNA; 25 BP.

AC AAX78994;

DT 17-AUG-1999 (first entry)

XX Oligonucleotide #60 for recombination and cloning method.

DE Cloning; donor; recombination site; vector; chimeric; ss.

XX Synthetic.

OS WO9921977-A1.

XX 06-MAY-1999.

XX 26-OCT-1998; 98WO-US022589.

XX 24-OCT-1997; 97US-0065930P.

PR 23-OCT-1998; 98US-00177387.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Fox DK;

PI WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

PT Disclosure; Page 176; 185pp; English.

PS The invention relates to novel methods for cloning or subcloning one or  
XX more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
XX in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
XX more desired nucleic acid segments flanked by at least 2 recombination  
XX sites which do not recombine with each other; (2) one or more vector  
XX donor molecules (VDMs) comprising at least 2 recombination sites which do  
XX not recombine with each other; and (3) one or more site-specific  
XX recombination proteins; (b) incubating the combination to transfer one or  
XX more of the desired segments into one or more of the VDMs, thereby  
XX producing one or more desired product molecules (PMS). The methods can be  
XX used for the efficient and specific recombination of NAM segments. They  
XX can be used to generate chimeric DNA or RNA molecules that have the  
XX desired characteristics and/or nucleic acid segments. The methods can  
XX also be used for changing vectors. The oligonucleotides AAX78935-X78994  
XX are used in the method of the invention

XX Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 2; Length 25;  
Best Local Similarity 60.0%; Pred. No. 28;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
Db 1 AGCCTGCTTTTATATACTAATTGA 25

## RESULT 13

AAX78977  
ID AAX78977 standard; DNA; 25 BP.

XX AAX78977;

XX 17-AUG-1999 (first entry)

XX Oligonucleotide #43 for recombination and cloning method.

DE Cloning; donor; recombination site; vector; chimeric; ss.

XX Synthetic.

XX WO9921977-A1.

XX 06-MAY-1999.

XX 26-OCT-1998; 98WO-US022589.

XX 24-OCT-1997; 97US-0065930P.

PR 23-OCT-1998; 98US-00177387.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Fox DK;

PI WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

PS Disclosure; Page 171; 185pp; English.

XX The invention relates to novel methods for cloning or subcloning one or  
XX more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
XX in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
XX more desired nucleic acid segments flanked by at least 2 recombination  
XX sites which do not recombine with each other; (2) one or more vector  
XX donor molecules (VDMs) comprising at least 2 recombination sites which do  
XX not recombine with each other; and (3) one or more site-specific  
XX recombination proteins; (b) incubating the combination to transfer one or  
XX more of the desired segments into one or more of the VDMs, thereby  
XX producing one or more desired product molecules (PMS). The methods can be  
XX used for the efficient and specific recombination of NAM segments. They  
XX can be used to generate chimeric DNA or RNA molecules that have the  
XX desired characteristics and/or nucleic acid segments. The methods can  
XX also be used for changing vectors. The oligonucleotides AAX78935-X78994  
XX are used in the method of the invention

XX Sequence 25 BP; 4 A; 3 C; 5 G; 10 T; 0 U; 3 Other;  
Query Match 80.8%; Score 20.2; DB 2; Length 25;  
Best Local Similarity 72.0%; Pred. No. 28;  
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
Db 1 GTTCAGCTTTTTRTACWAAAGTTGG 25

## RESULT 14

AAX78940  
ID AAX78940 standard; DNA; 25 BP.

XX

```

AC AAX78940;
XX 17-AUG-1999 (first entry)
XX DT
XX DE Oligonucleotide #6 for recombination and cloning method.
XX KW Cloning; donor; recombination site; vector; chimeric; ss.
XX OS Synthetic.
XX PN WO9921977-A1.
XX PD 06-MAY-1999.
XX PF 26-OCT-1998; 98WO-US022589.
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX WPI; 1999-303011/25.
XX PR New nucleic acid cloning methods.
XX PS Disclosure; Page 160; 185pp; English.
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;
XX
Query Match 80.8%; Score 20.2; DB 2; Length 25;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RBYCWCCTTTTTRTACWAASTKGD 25
Db 1 AGCTGCTTTTGTACAACTTGT 25
RESULT 15
AAX78942
ID AAX78942 standard; DNA; 25 BP.
XX AC
XX AC AAX78942;
XX DT
XX DT 17-AUG-1999 (first entry)
XX DE Oligonucleotide #8 for recombination and cloning method.
XX KW Cloning; donor; recombination site; vector; chimeric; ss.
XX OS Synthetic.
XX PN WO9921977-A1.
XX PD 06-MAY-1999.
XX PF 26-OCT-1998; 98WO-US022589.
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX WPI; 1999-303011/25.
XX PR New nucleic acid cloning methods.
XX PS Disclosure; Page 160; 185pp; English.
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;
XX
Query Match 80.8%; Score 20.2; DB 2; Length 25;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RBYCWCCTTTTTRTACWAASTKGD 25
Db 1 AGCTGCTTTTGTACAACTTGT 25

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Job time : 167.8 secs

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds  
(without alignments)  
494.978 Million cell updates/sec

Title: US-10-820-133-39

Perfect score: 25

Sequence: 1 rbycggttcttctacwaastkgd 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20.2	80.8	25	3	US-09-233-493-7
3	20.2	80.8	25	3	US-09-233-493-8
4	20.2	80.8	25	3	US-09-233-493-9
5	20.2	80.8	25	3	US-09-233-493-10
6	20.2	80.8	25	3	US-09-233-493-11
7	20.2	80.8	25	3	US-09-233-493-12
8	20.2	80.8	25	3	US-09-233-493-13
9	20.2	80.8	25	3	US-09-233-493-14
10	20.2	80.8	25	3	US-09-233-493-15
11	20.2	80.8	25	3	US-09-233-493-16
12	20.2	80.8	25	3	US-09-233-493-31
13	20.2	80.8	25	3	US-09-233-493-32
14	20.2	80.8	25	3	US-09-233-493-33
15	20.2	80.8	25	3	US-09-233-493-34
16	20.2	80.8	25	3	US-09-233-493-35
17	20.2	80.8	25	3	US-09-005-476-6
18	20.2	80.8	25	3	US-09-005-476-7
19	20.2	80.8	25	3	US-09-005-476-8
20	20.2	80.8	25	3	US-09-005-476-9
21	20.2	80.8	25	3	US-09-005-476-10
22	20.2	80.8	25	3	US-09-005-476-11
23	20.2	80.8	25	3	US-09-005-476-12
24	20.2	80.8	25	3	US-09-005-476-13
25	20.2	80.8	25	3	US-09-005-476-14
26	20.2	80.8	25	3	US-09-005-476-15
27	20.2	80.8	25	3	US-09-005-476-16

Sequence 31, Appl  
Sequence 32, Appl  
Sequence 33, Appl  
Sequence 34, Appl  
Sequence 35, Appl  
Sequence 6, Appl  
Sequence 7, Appl  
Sequence 8, Appl  
Sequence 9, Appl  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 15, Appl  
Sequence 16, Appl  
Sequence 31, Appl  
Sequence 32, Appl

28 20.2 80.8 25 3 US-09-005-476-31  
c 29 20.2 80.8 25 3 US-09-005-476-32  
c 30 20.2 80.8 25 3 US-09-005-476-33  
c 31 20.2 80.8 25 3 US-09-005-476-34  
c 32 20.2 80.8 25 3 US-09-005-476-35  
33 20.2 80.8 25 3 US-09-233-492-6  
34 20.2 80.8 25 3 US-09-233-492-7  
35 20.2 80.8 25 3 US-09-233-492-8  
36 20.2 80.8 25 3 US-09-233-492-9  
37 20.2 80.8 25 3 US-09-233-492-10  
38 20.2 80.8 25 3 US-09-233-492-11  
39 20.2 80.8 25 3 US-09-233-492-12  
40 20.2 80.8 25 3 US-09-233-492-13  
41 20.2 80.8 25 3 US-09-233-492-14  
42 20.2 80.8 25 3 US-09-233-492-15  
43 20.2 80.8 25 3 US-09-233-492-16  
44 20.2 80.8 25 3 US-09-233-492-31  
c 45 20.2 80.8 25 3 US-09-233-492-32

## ALIGNMENTS

RESULT 1  
US-09-233-493-6  
; Sequence 6, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
US-09-233-493-6

Query Match 80.8%; Score 20.2; DB 3; Length 25;  
 Best Local Similarity 60.0%; Pred. No. 4.5;  
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
 Db 1 AGCCTGCTTTTGTGACAACTTGT 25

## RESULT 2

US-09-233-493-7  
 ; Sequence 7, Application US/09233493  
 ; Patent No. 6143557  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hartley, James L.  
 ; APPLICANT: Brasch, Michael A.  
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
 ; TITLE OF INVENTION: Recombination Sites  
 ; NUMBER OF SEQUENCES: 35  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
 ; STREET: 1100 New York Ave., N. W. Suite 600  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA

ZIP: 20005-3934  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/233,493  
 ; FILING DATE: 20-JAN-1999  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/005,476  
 ; FILING DATE: 12-JAN-1998

CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/663,002  
 ; FILING DATE: 07-JUN-1996  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486,139  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION:  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 25 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: both  
 ; MOLECULE TYPE: cdna  
 ; US-09-233-493-7

Query Match 80.8%; Score 20.2; DB 3; Length 25;  
 Best Local Similarity 60.0%; Pred. No. 4.5;  
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
 Db 1 AGCCTGCTTTTGTGACAACTTGT 25

## RESULT 3

US-09-233-493-8  
 ; Sequence 8, Application US/09233493  
 ; Patent No. 6143557  
 ; GENERAL INFORMATION:

APPLICANT: Hartley, James L.  
 ; APPLICANT: Brasch, Michael A.  
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
 ; TITLE OF INVENTION: Recombination Sites  
 ; NUMBER OF SEQUENCES: 35  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
 ; STREET: 1100 New York Ave., N. W. Suite 600  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA

ZIP: 20005-3934  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/233,493  
 ; FILING DATE: 20-JAN-1999  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/005,476  
 ; FILING DATE: 12-JAN-1998

CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/663,002  
 ; FILING DATE: 07-JUN-1996  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/486,139  
 ; FILING DATE: 07-JUN-1995

CLASSIFICATION:  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-2600  
 ; TELEFAX: 202-371-2540  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 25 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: both  
 ; MOLECULE TYPE: cdna  
 ; US-09-233-493-8

Query Match 80.8%; Score 20.2; DB 3; Length 25;  
 Best Local Similarity 60.0%; Pred. No. 4.5;  
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
 Db 1 ACCGAGCTTTCTTGTCACAACTTGT 25

## RESULT 4

US-09-233-493-9  
 ; Sequence 9, Application US/09233493  
 ; Patent No. 6143557  
 ; GENERAL INFORMATION:

APPLICANT: Hartley, James L.  
 ; APPLICANT: Brasch, Michael A.  
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
 ; TITLE OF INVENTION: Recombination Sites  
 ; NUMBER OF SEQUENCES: 35  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
 ; STREET: 1100 New York Ave., N. W. Suite 600  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA

ZIP: 20005-3934  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/233,493  
FILING DATE: 20-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,476  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cdna  
US-09-233-493-9

Query Match 80.8%; Score 20.2; DB 3; Length 25;  
Best Local Similarity 60.0%; Pred. No. 4.5;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWCCTTTTTRTACWAASTKGD 25  
:::|||||:::|||||:::|||||:::|||||:::|||||:::  
Db 1 GTTCAGCTTTTGTGACAAACTTGT 25

RESULT 5  
US-09-233-493-10  
Sequence 10, Application US/09233493  
Patent No. 6143557  
GENERAL INFORMATION:  
APPLICANT: Hartley, James L.  
APPLICANT: Brasch, Michael A.  
TITLE OF INVENTION: Recombinational Cloning Using Engineered  
TITLE OF INVENTION: Recombination Sites  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
STREET: 1100 New York Ave., N. W. Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/233,493  
FILING DATE: 20-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,476  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cdna  
US-09-233-493-10  
Query Match 80.8%; Score 20.2; DB 3; Length 25;  
Best Local Similarity 60.0%; Pred. No. 4.5;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RBYCWCCTTTTTRTACWAASTKGD 25  
:::|||||:::|||||:::|||||:::|||||:::|||||:::  
Db 1 GTTCAGCTTTTGTGACAAACTTGT 25  
RESULT 6  
US-09-233-493-11  
Sequence 11, Application US/09233493  
Patent No. 6143557  
GENERAL INFORMATION:  
APPLICANT: Hartley, James L.  
APPLICANT: Brasch, Michael A.  
TITLE OF INVENTION: Recombinational Cloning Using Engineered  
TITLE OF INVENTION: Recombination Sites  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
STREET: 1100 New York Ave., N. W. Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/233,493  
FILING DATE: 20-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,476  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,139  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both

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; MOLECULE TYPE: cdna
US-09-233-493-11

Query Match      80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
   :|||:||||:||||:||||:||||:||||:
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 7
US-09-233-493-12
; Sequence 12, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-12

Query Match      80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
   :|||:||||:||||:||||:||||:||||:
Db 1 AGCCTGCTTTTGTACAAAGTTGG 25

RESULT 8
US-09-233-493-13

Query Match      80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
   :|||:||||:||||:||||:||||:||||:
Db 1 AGCCTGCTTTTGTACAAAGTTGG 25
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; Sequence 13, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-13

Query Match      80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
   :|||:||||:||||:||||:||||:||||:
Db 1 AGCCTGCTTCTTGTACAAAGTTGG 25

RESULT 9
US-09-233-493-14
; Sequence 14, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
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;; ZIP: 20005-3934  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA: US/09/233,493  
;; FILING DATE: 20-JAN-1999  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/005,476  
;; FILING DATE: 12-JAN-1998  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/663,002  
;; FILING DATE: 07-JUN-1996  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/486,139  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2540  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; MOLECULE TYPE: cdna  
US-09-233-493-14

Query Match 80.8%; Score 20.2; DB 3; Length 25;  
Best Local Similarity 60.0%; Pred. No. 4.5;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCGCTTTTTRTACMAASTKGD 25  
:::|||||:|||||:|||||:|||||:  
Db 1 ACCGAGCTTCTTGACAAAGTTGG 25

RESULT 10  
US-09-233-493-15  
;; Sequence 15, Application US/09233493  
;; Patent No. 6143557  
;; GENERAL INFORMATION:  
;; APPLICANT: Hartley, James L.  
;; APPLICANT: Brasch, Michael A.  
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
;; TITLE OF INVENTION: Recombination Sites  
;; NUMBER OF SEQUENCES: 35  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
;; STREET: 1100 New York Ave., N. W. Suite 600  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005-3934  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/233,493  
;; FILING DATE: 20-JAN-1999  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/005,476  
;; FILING DATE: 12-JAN-1998  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/663,002  
;; FILING DATE: 07-JUN-1996  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/486,139  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 16:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/663,002  
;; FILING DATE: 07-JUN-1996  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/486,139  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; MOLECULE TYPE: cdna  
US-09-233-493-15

Query Match 80.8%; Score 20.2; DB 3; Length 25;  
Best Local Similarity 60.0%; Pred. No. 4.5;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCGCTTTTTRTACMAASTKGD 25  
:::|||||:|||||:|||||:|||||:  
Db 1 GTTCAGCTTTTGTGACAAAGTTGG 25

RESULT 11  
US-09-233-493-16  
;; Sequence 16, Application US/09233493  
;; Patent No. 6143557  
;; GENERAL INFORMATION:  
;; APPLICANT: Hartley, James L.  
;; APPLICANT: Brasch, Michael A.  
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
;; TITLE OF INVENTION: Recombination Sites  
;; NUMBER OF SEQUENCES: 35  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
;; STREET: 1100 New York Ave., N. W. Suite 600  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005-3934  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/233,493  
;; FILING DATE: 20-JAN-1999  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/005,476  
;; FILING DATE: 12-JAN-1998  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/663,002  
;; FILING DATE: 07-JUN-1996  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/486,139  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 16:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs

;  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
US-09-233-493-16

Query Match 80.8%; Score 20.2; DB 3; Length 25;  
Best Local Similarity 60.0%; Pred. No. 4.5;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCGCTTTTTRTACWAASTKGD 25  
:::|||||:|||||:|||||:|||||:|:  
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 12  
US-09-233-493-31  
; Sequence 31, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
US-09-233-493-31

Query Match 80.8%; Score 20.2; DB 3; Length 25;  
Best Local Similarity 60.0%; Pred. No. 4.5;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCGCTTTTTRTACWAASTKGD 25  
:::|||||:|||||:|||||:|||||:|:  
Db 1 AGCTGCTTTTATATACTAATTGA 25

RESULT 13  
US-09-233-493-32/c  
; Sequence 32, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
US-09-233-493-32

Query Match 80.8%; Score 20.2; DB 3; Length 25;  
Best Local Similarity 60.0%; Pred. No. 4.5;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCGCTTTTTRTACWAASTKGD 25  
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Db 25 AGCTGCTTTTATATACTAATTGA 1

RESULT 14  
US-09-233-493-33/c  
; Sequence 33, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600

; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
; US-09-233-493-33

Query Match 80.8%; Score 20.2; DB 3; Length 25;  
Best Local Similarity 60.0%; Pred. No. 4.5;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBVCGCTTTTTRTACWAASTKGD 25  
Db :::::|||||:|||||:|||||:|  
25 AGCCTGCTTTTGTACAAACTTGT 1

## RESULT 15

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; Sequence 34, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
; US-09-233-493-34

Query Match 80.8%; Score 20.2; DB 3; Length 25;  
Best Local Similarity 60.0%; Pred. No. 4.5;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBVCGCTTTTTRTACWAASTKGD 25  
Db :::::|||||:|||||:|||||:|  
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Search completed: November 16, 2004, 10:22:31  
Job time : 35.9 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 ; Search time 314 Seconds  
(without alignments)  
430.015 Million cell updates/sec

Title: US-10-820-133-39

Perfect score: 25  
Sequence: 1 rbycwgcttcttctacwaastkqd 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
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- 18: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20.2	80.8	25	9	US-09-732-914-9
4	20.2	80.8	25	9	US-09-732-914-12
5	20.2	80.8	25	9	US-09-732-914-95
6	20.2	80.8	25	9	US-09-855-797A-6
7	20.2	80.8	25	9	US-09-855-797A-7
8	20.2	80.8	25	9	US-09-855-797A-8
9	20.2	80.8	25	9	US-09-855-797A-9
10	20.2	80.8	25	9	US-09-855-797A-10
11	20.2	80.8	25	9	US-09-855-797A-11
12	20.2	80.8	25	9	US-09-855-797A-12

13	20.2	80.8	25	9	US-09-855-797A-13	Sequence 13, Appl
14	20.2	80.8	25	9	US-09-855-797A-14	Sequence 14, Appl
15	20.2	80.8	25	9	US-09-855-797A-15	Sequence 15, Appl
16	20.2	80.8	25	9	US-09-855-797A-16	Sequence 16, Appl
17	20.2	80.8	25	9	US-09-855-797A-39	Sequence 39, Appl
18	20.2	80.8	25	9	US-09-855-797A-40	Sequence 40, Appl
19	20.2	80.8	25	9	US-09-855-797A-41	Sequence 41, Appl
20	20.2	80.8	25	9	US-09-855-797A-42	Sequence 42, Appl
21	20.2	80.8	25	9	US-09-855-797A-43	Sequence 43, Appl
22	20.2	80.8	25	9	US-09-855-797A-60	Sequence 60, Appl
23	20.2	80.8	25	9	US-09-822-634-8	Sequence 8, Appl
24	20.2	80.8	25	9	US-09-822-634-9	Sequence 9, Appl
25	20.2	80.8	25	9	US-09-822-634-10	Sequence 10, Appl
26	20.2	80.8	25	9	US-09-822-634-11	Sequence 11, Appl
27	20.2	80.8	25	9	US-09-907-900-6	Sequence 6, Appl
28	20.2	80.8	25	9	US-09-907-900-7	Sequence 7, Appl
29	20.2	80.8	25	9	US-09-907-900-8	Sequence 8, Appl
30	20.2	80.8	25	9	US-09-907-900-9	Sequence 9, Appl
31	20.2	80.8	25	9	US-09-907-900-10	Sequence 10, Appl
32	20.2	80.8	25	9	US-09-907-900-11	Sequence 11, Appl
33	20.2	80.8	25	9	US-09-907-900-12	Sequence 12, Appl
34	20.2	80.8	25	9	US-09-907-900-13	Sequence 13, Appl
35	20.2	80.8	25	9	US-09-907-900-14	Sequence 14, Appl
36	20.2	80.8	25	9	US-09-907-900-15	Sequence 15, Appl
37	20.2	80.8	25	9	US-09-907-900-16	Sequence 16, Appl
38	20.2	80.8	25	9	US-09-907-900-39	Sequence 39, Appl
39	20.2	80.8	25	9	US-09-907-900-40	Sequence 40, Appl
40	20.2	80.8	25	9	US-09-907-900-41	Sequence 41, Appl
41	20.2	80.8	25	9	US-09-907-900-42	Sequence 42, Appl
42	20.2	80.8	25	9	US-09-907-900-43	Sequence 43, Appl
43	20.2	80.8	25	9	US-09-907-900-60	Sequence 60, Appl
44	20.2	80.8	25	9	US-09-907-719-6	Sequence 6, Appl
45	20.2	80.8	25	9	US-09-907-719-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-09-732-914-5  
; Sequence 5, Application US/09732914  
; Patent No. US20020007051A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheo, David  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Hartley, James L.  
; APPLICANT: Byrd, Devon R.N.  
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in  
; FILE REFERENCE: 0942.5010002  
; CURRENT APPLICATION NUMBER: US/09/732.914  
; CURRENT FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 60/169,983  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: US 60/188,020  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: attB1  
US-09-732-914-5

Query Match 80.8%; Score 20.2; DB 9; Length 25;  
Best Local Similarity 60.0%; Pred. No.19;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RBYCWCCTTTTCTTACWAASTKGD 25  
Db 1 AGCTGCTTTTGTACAACTTGT 25

## RESULT 2

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US-09-732-914-8
; Sequence 8, Application US/09732914
; Patent No. US2002007051A1
; GENERAL INFORMATION:
; APPLICANT: Celo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multimeric
; TITLE OF INVENTION: Recombination
; FILE REFERENCE: 0942.501002
; CURRENT APPLICATION NUMBER: US/09/09-732-914-8
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr1
US-09-732-914-8

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Query Match 80.8%; Score 20.2; DB 9; Length 25;  
Best Local Similarity 60.0%; Pred. No. 19;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 RBYCWGCTTYYTRTACWAASTKGD 25  
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**Db** 1 GTTCAGCTTTTGTACAAACTGT 25

### RESULT 3

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US-09-732-914-9
; Sequence 9, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multi-
; TITLE OF INVENTION: Recombination
; FILE REFERENCE: 0942.501002
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attB2
US-09-732-914-9

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Best Local Similarity 60.0%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
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**Qy** 1 RBYCWGCTTTYTRTACWAATKGD 25  
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**Db** 1 ACCCAGCTTCTTGTCACAAAGTGGT 25

## RESULT 6

## RESULT 4

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US-09-732-914-12
; Sequence 12, Application US/09732914
; Patent No. US2002007051A1
; GENERAL INFORMATION:
; APPLICANT: Chesco, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multipip
; TITLE OF INVENTION: Recombinationa
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/0973
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/1
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/1
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr2
US-09-732-914-12

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Query Match      80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
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**Qy**

1 RBYCWGCTTTTYYTRTACWAASTKGD 25  
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**pb**

1 GTTCAGCTTCTCGTACAAAGTGGT 25

## RESULT 5

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; Sequence 95, Application US/09732914
; Patent No. US2002007051A1
; GENERAL INFORMATION:
; APPLICANT: Chao, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multipip
; TITLE OF INVENTION: Recombinationa
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/77
; CURRENT FILING DATE: 2000-12-11
; PRIORITY APPLICATION NUMBER: US 60/1
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/1
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attB0
US-09-732-914-95

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Query Match 80.8%; Score 20.2; DB 9; Length 25;  
Best Local Similarity 60.0%; Pred. No. 19;  
Matches 15: Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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**pB**

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; Sequence 6, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-6

Query Match          80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No.19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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DB      1  AGCTGCTTTTGTACAACTTGT 25

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US-09-855-797A-7
; Sequence 7, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-7

Query Match          80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No.19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY      1  RBYCWGCTTTTTRTACWAASTKGD 25
DB      1  AGCTGCTTTTGTACAACTTGT 25

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RESULT 8
US-09-855-797A-8
; Sequence 8, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-855-797A-8

Query Match          80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps

Qy      1  RBYCWGCTTTTTRTACWAASATKGD 25
Db      1  ACCCAGCTTCTTGACAAAGTGT 25

RESULT 9
US-09-855-797A-9
; Sequence 9, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
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; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-855-797A-9

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Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTTCTGTACAAACTTGT 25

## RESULT 10

US-09-855-797A-10  
; Sequence 10, Application US/09855797A  
; Patent No. US20020094574A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850008  
; CURRENT APPLICATION NUMBER: US/09/855,797A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/296,281  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-855-797A-10

Query Match 80.8%; Score 20.2; DB 9; Length 25;  
Best Local Similarity 60.0%; Pred. No. 19;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
:::|||||:|||||:|||||:|||||:  
Db 1 GTTCAGCTTTTCTGTACAAACTTGT 25

## RESULT 11

US-09-855-797A-11  
; Sequence 11, Application US/09855797A  
; Patent No. US20020094574A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850008  
; CURRENT APPLICATION NUMBER: US/09/855,797A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/296,281  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-855-797A-11

Query Match 80.8%; Score 20.2; DB 9; Length 25;

Best Local Similarity 60.0%; Pred. No. 19;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
:::|||||:|||||:|||||:|||||:  
Db 1 GTTCAGCTTTTCTGTACAAAGTGT 25

## RESULT 12

US-09-855-797A-12  
; Sequence 12, Application US/09855797A  
; Patent No. US20020094574A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850008  
; CURRENT APPLICATION NUMBER: US/09/855,797A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/296,281  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin Ver. 2.0  
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; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-855-797A-12

Query Match 80.8%; Score 20.2; DB 9; Length 25;  
Best Local Similarity 60.0%; Pred. No. 19;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
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Db 1 AGCTGCTTTTGTGACAAAGTTGG 25

## RESULT 13

US-09-855-797A-13  
; Sequence 13, Application US/09855797A  
; Patent No. US20020094574A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850008  
; CURRENT APPLICATION NUMBER: US/09/855,797A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/296,281  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-855-797A-13

; ORGANISM: Unknown

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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(without alignments)  
594.643 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: gb\_est5:  
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8: gb\_g8a1:  
9: gb\_g8a2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	20.2	80.8	83	CB401650	CB401650 OSTF197D3
5	20.2	80.8	84	CB400948	CB400948 OSTF185C6
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29	20.2	80.8	95	7	CF652333	CF652333 49-L02013
30	20.2	80.8	95	7	CF652453	CF652453 56-L02052
31	20.2	80.8	95	7	CF652502	CF652502 59-L02052
32	20.2	80.8	95	7	CF652546	CF652546 62-L02036
33	20.2	80.8	95	7	CF652555	CF652555 62-L02057
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39	20.2	80.8	95	7	CF652698	CF652698 71-L02036
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43	20.2	80.8	95	7	CF652855	CF652855 80-L02058
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

CF651937 79 bp mRNA linear EST 06-NOV-2003  
24-L020167-066-001-P06-SP6P MP1Z-ADIS-066 Arabidopsis thaliana cDNA  
Clone MP1Zp2001P061Q 5-PRIME, mRNA sequence.

CF651937  
CF651937.1 GI:37427952  
EST.  
Arabidopsis thaliana (thale cress)

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 79)  
Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T.,  
Mitchell-Olds, T. and Weishaar, B.  
Large-scale identification and analysis of genome-wide  
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana  
Genome Res. 13 (6), 1250-1257 (2003)

22683290  
12799357  
Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
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was made at the Max-Planck-Institute for Plant Breeding  
Research, Cologne, Germany; cloning sites SalI-NotI,

primer sites and orientation:  
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## ORIGIN

Query Match 80.8%; Score 20.2; DB 7; Length 79;  
 Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
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 Db 48 ACCCAGCTTTCTGTACAAAGTGGT 72

## RESULT 2

CB394681/c CB394681 80 bp mRNA linear EST 15-MAY-2003  
 DEFINITION OSTR142B12\_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.  
 ACCESSION CB394681

VERSION CB394681.1 GI:30736392

## KEYWORDS

EST.

## SOURCE

Caenorhabditis elegans  
 Caenorhabditis elegans  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

## REFERENCE

1 (bases 1 to 80)

## AUTHORS

Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,  
 Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,  
 Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,  
 Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,  
 Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,  
 Doucette-Stamm,L., Hill,D.E. and Vidal,M.

## TITLE

C. elegans ORFeome version 1.1: experimental verification of the  
 genome annotation and resource for proteome-scale protein  
 expression

## JOURNAL

Nat. Genet. (2003) In press

## COMMENT

Contact: Vidal M  
 Dana Farber Cancer Institute  
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
 Tel: 617 632 5180  
 Fax: 617 632 5739

Email: [Marc.Vidal@dfci.harvard.edu](mailto:Marc.Vidal@dfci.harvard.edu)  
 Sequence tag of Gateway entry clones. The primers used were  
 designed on the predicted protein encoding ORF. C. elegans ORFeome  
 cloning project : Contact [david\\_hill@dfci.harvard.edu](mailto:david_hill@dfci.harvard.edu) or  
[marc\\_vidal@dfci.harvard.edu](mailto:marc_vidal@dfci.harvard.edu)  
 POLYA=No.

## FEATURES

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/note="The AD-wrmcDNA library was generated with poly(A)+  
 RNA isolated from both hermaphrodite and male N2 worms of  
 all larval stages, embryos, adults and dauers and the  
 subsequent generation of cDNAs by poly(A) priming. The  
 cDNAs were cloned into pPC86"

## ORIGIN

Query Match 80.8%; Score 20.2; DB 6; Length 80;

Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25

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 Db 55 ACCCAGCTTTCTGTACAAAGTGGT 31

## RESULT 3

## CB398074

LOCUS CB398074 83 bp mRNA linear EST 15-MAY-2003  
 DEFINITION OSTR197D3\_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.  
 ACCESSION CB398074

VERSION CB398074.1 GI:30739801

## KEYWORDS

EST.

## SOURCE

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

## REFERENCE

1 (bases 1 to 83)

## AUTHORS

Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,  
 Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,  
 Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,  
 Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,  
 Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,  
 Doucette-Stamm,L., Hill,D.E. and Vidal,M.

C. elegans ORFeome version 1.1: experimental verification of the  
 genome annotation and resource for proteome-scale protein  
 expression

## JOURNAL

Nat. Genet. (2003) In press

## COMMENT

Contact: Vidal M  
 Marc Vidal Laboratory  
 Dana Farber Cancer Institute  
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
 Tel: 617 632 5180  
 Fax: 617 632 5739

Email: [Marc.Vidal@dfci.harvard.edu](mailto:Marc.Vidal@dfci.harvard.edu)

Sequence tag of Gateway entry clones. The primers used were  
 designed on the predicted protein encoding ORF. C. elegans ORFeome  
 cloning project : Contact [david\\_hill@dfci.harvard.edu](mailto:david_hill@dfci.harvard.edu) or  
[marc\\_vidal@dfci.harvard.edu](mailto:marc_vidal@dfci.harvard.edu)  
 POLYA=No.

## FEATURES

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/note="The AD-wrmcDNA library was generated with poly(A)+  
 RNA isolated from both hermaphrodite and male N2 worms of  
 all larval stages, embryos, adults and dauers and the  
 subsequent generation of cDNAs by poly(A) priming. The  
 cDNAs were cloned into pPC86"

## ORIGIN

Query Match 80.8%; Score 20.2; DB 6; Length 83;

Best Local Similarity 60.0%; Pred. No. 2.2e+02;

Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25

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 Db 33 AGCCTGCTTTTCTGTACAAAGTGGT 57

## RESULT 4

## CB401650/c

LOCUS CB401650 83 bp mRNA linear EST 15-MAY-2003  
 DEFINITION OSTR197D3\_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.  
 ACCESSION CB401650

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VERSION          CB401650.1  GI:30743377
KEYWORDS         EST.
SOURCE           Caenorhabditis elegans
ORGANISM         Caenorhabditis elegans
REFERENCE        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
AUTHORS          Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                  1 (bases 1 to 83)
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL          Nat. Genet. (2003) In press
COMMENT          Contact: Vidal M
                  Marc Vidal Laboratory
                  Dana Farber Cancer Institute
                  1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
                  Tel: 617 632 5180
                  Fax: 617 632 5739
                  Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

TITLE           C. elegans ORFome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL          Nat. Genet. (2003) In press
COMMENT          Contact: Vidal M
                  Marc Vidal Laboratory
                  Dana Farber Cancer Institute
                  1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
                  Tel: 617 632 5180
                  Fax: 617 632 5739
                  Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

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                 /tissue_type="whole animal"
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                 /note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

ORIGIN           Query Match      80.8%; Score 20.2; DB 6; Length 83;
                 Best Local Similarity 60.0%; Pred. No. 2.2e+02;
                 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              1 RBYCWGCTTTTTRTACWAASAKGD 25
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Db              51 AGCGTGCTTTTGTGACAACTTGT 27
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RESULT 5
CB400948        84 bp mRNA linear EST 15-MAY-2003
LOCUS           OSTF185C6_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
DEFINITION      CB400948
ACCESSION       CB400948
VERSION         CB400948.1  GI:30742675
KEYWORDS        EST.
SOURCE          Caenorhabditis elegans
ORGANISM        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                 Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                 1 (bases 1 to 84)
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL          Nat. Genet. (2003) In press
COMMENT          Contact: Vidal M
                  Marc Vidal Laboratory
                  Dana Farber Cancer Institute
                  1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
                  Tel: 617 632 5180
                  Fax: 617 632 5739
                  Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES         Location/Qualifiers
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

ORIGIN           Query Match      80.8%; Score 20.2; DB 6; Length 84;
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                 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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Db              35 ACCAGCTTTTCTGTACAAAGTGGG 59
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RESULT 6
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DEFINITION      CB400039
ACCESSION       CB400039
VERSION         CB400039.1  GI:30741766
KEYWORDS        EST.
SOURCE          Caenorhabditis elegans
ORGANISM        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                 Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                 1 (bases 1 to 87)
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL          Nat. Genet. (2003) In press
COMMENT          Contact: Vidal M
                  Marc Vidal Laboratory
                  Dana Farber Cancer Institute
                  1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
                  Tel: 617 632 5180
                  Fax: 617 632 5739
                  Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

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cloning project : Contact david\_hill@fci.harvard.edu or  
marc.vidal@fci.harvard.edu  
POLYA-No.

FEATURES source Location/Qualifiers

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/mol_type="mRNA"
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/dev_stages="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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# ORIGIN

Query Match 80.8%; Score 20.2; DB 6; Length 87;  
Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
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Db 30 ACCCAGCTTCTTGTCACAAAGTTGG 6

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DEFINITION  
80-L020166-066-001-P19-SP6P MP1Z-ADIS-066 Arabidopsis thaliana cDNA  
clone MP1Zp2001P191Q 5-PRIME, mRNA sequence.

ACCESSION  
CF652842  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
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FEATURES source Location/Qualifiers

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cDNA library from Arabidopsis thaliana, accession
Wasilewskija-0; roots from three weeks old plants grown
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on MS-plates at 26M-0C with 16 hours light/day; library  
was made at the Max-Planck-Institute for Plant Breeding  
Research, Cologne, Germany; cloning sites SalI-NotI,  
primer sites and orientation:

SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY  
compatible; Note: Sequencing granted in the context of the  
GABI Arabidopsis Verbund I: Genetic Diversity,  
'Establishment of high-efficiency SNP-based mapping tools  
and development of methods for genome-wide mutation  
detection' PI: Bernd Weisshaar Sequence submission managed  
by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This  
clone is available from RZPD; contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de))  
for further information."

# ORIGIN

Query Match 80.8%; Score 20.2; DB 7; Length 87;  
Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RBYCWGCTTTTTRTACWAASTKGD 25  
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Db 44 ACCCAGCTTCTTGTCACAAAGTTGG 68

RESULT 8  
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19-L020524-066-003-E06-SP6P MP1Z-ADIS-066 Arabidopsis thaliana cDNA  
clone MP1Zp2001E063Q 5-PRIME, mRNA sequence.

ACCESSION  
CF651862  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
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FEATURES source Location/Qualifiers

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/clone_lib="MP1Z-ADIS-066"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from Arabidopsis thaliana, accession
Wasilewskija-0; roots from three weeks old plants grown
on MS-plates at 26M-0C with 16 hours light/day; library
was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites SalI-NotI,
primer sites and orientation:
SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY
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compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

## ORIGIN

Query Match 80.8%; Score 20.2; DB 7; Length 89;  
Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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Db 44 ACCCAGCTTCTTGTACAAAGTGT 68

RESULT 9  
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CF652759  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

1 (bases 1 to 89)  
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,  
Mitchell-Olds,T. and Weisshaar,B.  
Large-scale identification and analysis of genome-wide  
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana  
Genome Res. 13 (6), 1250-1257 (2003)  
22683290  
12799357

Contact: Weisshaar B  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
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FEATURES  
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CDNA library from Arabidopsis thaliana, accession  
Wassilewskija-0; roots from three weeks old plants grown  
on MS-plates at 26M-OC with 16 hours light/day; library  
was made at the Max-Planck-Institute for Plant Breeding  
Research, Cologne, Germany; Cloning sites SalI-NotI,  
primer sites and orientation:  
SP6-Sali-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY  
compatible; Note: Sequencing granted in the context of the  
GABI Arabidopsis Verbund I: Genetic Diversity,  
'Establishment of high-efficiency SNP-based mapping tools  
and development of methods for genome-wide mutation  
detection' PI: Bernd Weisshaar Sequence submission managed

by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

## ORIGIN

Query Match 80.8%; Score 20.2; DB 7; Length 89;  
Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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Db 44 ACCCAGCTTCTTGTACAAAGTGT 68

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CF653076  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

1 (bases 1 to 89)  
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,  
Mitchell-Olds,T. and Weisshaar,B.  
Large-scale identification and analysis of genome-wide  
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana  
Genome Res. 13 (6), 1250-1257 (2003)  
22683290  
12799357

Contact: Weisshaar B  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
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FEATURES  
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/clone\_lib="MP12-ADIS-066"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
CDNA library from Arabidopsis thaliana, accession  
Wassilewskija-0; roots from three weeks old plants grown  
on MS-plates at 26M-OC with 16 hours light/day; library  
was made at the Max-Planck-Institute for Plant Breeding  
Research, Cologne, Germany; Cloning sites SalI-NotI,  
primer sites and orientation:  
SP6-Sali-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY  
compatible; Note: Sequencing granted in the context of the  
GABI Arabidopsis Verbund I: Genetic Diversity,  
'Establishment of high-efficiency SNP-based mapping tools  
and development of methods for genome-wide mutation  
detection' PI: Bernd Weisshaar Sequence submission managed  
by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

## ORIGIN

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Query Match      80.8%; Score 20.2; DB 7; Length 89;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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Db 44 ACCCAGCTTCTGTACAAAGTGGT 68

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ACCESSION  CB392047
VERSION     CB392047.1 GI:30733757
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
REFERENCE  1 (bases 1 to 90)
AUTHORS    Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
            Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T.,
            Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
            Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V.,
            Tolia, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
            Doucette-Stamm, L., Hill, D.E. and Vidal, M.
TITLE      C. elegans ORFeome version 1.1: experimental verification of the
            genome annotation and resource for proteome-scale protein
            expression
JOURNAL    Nat. Genet. (2003) In press
COMMENT    Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc.Vidal@dfci.harvard.edu
            Sequence tag of Gateway entry clones. The primers used were
            designed on the predicted protein encoding ORF. C. elegans ORFeome
            cloning project : Contact david_hill@dfci.harvard.edu or
            marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES             Location/Qualifiers
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     dev_stage="mixed stage"
     clone_lib="AD-wrmcDNA"
     notes="The AD-wrmcDNA library was generated with poly(A)+
            RNA isolated from both hermaphrodite and male N2 worms of
            all larval stages, embryos, adults and dauers and the
            subsequent generation of cDNAs by poly(A) priming. The
            cDNAs were cloned into pPC86"

ORIGIN
Query Match      80.8%; Score 20.2; DB 6; Length 92;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
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DEFINITION Clone MP1Zp2001P201Q 5-PRIME, mRNA sequence.
ACCESSION  CF652843
VERSION     CF652843.1 GI:37429720
KEYWORDS   EST.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
REFERENCE  1 (bases 1 to 93)
AUTHORS    Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
            Mitchell-Olds, T. and Weishaar, B.
TITLE      Large-scale identification and analysis of genome-wide

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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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ORIGIN

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Job time : 1532 secs

GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:43 ; Search time 708.5 Seconds  
(without alignments)  
1668.656 Million cell updates/sec

Title: US-10-820-133-40

Perfect score: 25  
Sequence: 1 asccwgcttcttctacwaastkgw 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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GenEmbl.\*

1: gb\_ba.\*

2: gb\_hcg.\*

3: gb\_in.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	21.8	87.2	25	6	ARI24526 Sequence
2	21.8	87.2	25	6	ARI24527 Sequence
3	21.8	87.2	25	6	ARI24528 Sequence
4	21.8	87.2	25	6	ARI24551 Sequence
5	21.8	87.2	25	6	ARI24552 Sequence
6	21.8	87.2	25	6	ARI24553 Sequence
7	21.8	87.2	25	6	ARI24554 Sequence
8	21.8	87.2	25	6	ARI24555 Sequence
9	21.8	87.2	25	6	ARI24555 Sequence
10	21.8	87.2	25	6	ARI24555 Sequence
11	21.8	87.2	25	6	ARI24555 Sequence
12	21.8	87.2	25	6	ARI24555 Sequence
13	21.8	87.2	25	6	ARI24555 Sequence
14	21.8	87.2	25	6	ARI24555 Sequence
15	21.8	87.2	25	6	ARI24555 Sequence
16	21.8	87.2	25	6	ARI24555 Sequence
17	21.8	87.2	25	6	ARI24555 Sequence
18	21.8	87.2	25	6	ARI24555 Sequence
19	21.8	87.2	25	6	ARI24555 Sequence

20	21.8	87.2	25	6	AR493778	Sequence
21	21.8	87.2	25	6	AR493779	Sequence
22	21.8	87.2	25	6	AR493780	Sequence
23	21.8	87.2	25	6	AR493803	Sequence
c 24	21.8	87.2	25	6	AR493804	Sequence
c 25	21.8	87.2	25	6	AR493805	Sequence
c 26	21.8	87.2	25	6	AR493806	Sequence
c 27	21.8	87.2	25	6	AR493807	Sequence
c 28	21.8	87.2	25	6	AX127348	Sequence
c 29	21.8	87.2	25	6	AX127349	Sequence
30	21.8	87.2	25	6	AX491645	Sequence
31	21.8	87.2	25	6	AX491646	Sequence
32	21.8	87.2	25	6	AX491647	Sequence
33	21.8	87.2	25	6	AX491670	Sequence
34	21.8	87.2	25	6	AX498616	Sequence
35	21.8	87.2	25	6	AX498617	Sequence
36	21.8	87.2	25	6	AX498618	Sequence
37	21.8	87.2	25	6	AX498641	Sequence
c 38	21.8	87.2	25	6	AX787486	Sequence
c 39	21.8	87.2	25	6	AX787488	Sequence
40	21.8	87.2	25	6	AX787498	Sequence
41	21.8	87.2	25	6	AX787506	Sequence
42	21.8	87.2	25	6	AX787510	Sequence
43	21.8	87.2	25	6	BD131332	Recombina
44	21.8	87.2	25	6	BD131333	Recombina
45	21.8	87.2	25	6	BD131334	Recombina

## ALIGNMENTS

RESULT 1	ARI24526	ARI24526	Sequence 6 from patent US 6171861.	25 bp	DNA	linear	PAT 16-MAY-2001
LOCUS	ARI24526	Sequence 6 from patent US 6171861.					
DEFINITION	ARI24526	Sequence 6 from patent US 6171861.					
ACCESSION	ARI24526	Sequence 6 from patent US 6171861.					
VERSION	ARI24526.1	GI:14109887					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 25)						
AUTHORS	Hartley, J.L. and Brasch, M.A.						
TITLE	Recombinational cloning using engineered recombination sites						
JOURNAL	Patent: US 6171861-A 6 09-JAN-2001;						
FEATURES	Location/Qualifiers						
source	1..25						
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	/mol_type="unassigned DNA"						

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Matches 17;	Conservative 8;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ASCCWGCTTCTTCTACWAATKGW 25		
		: : : : : : : : : : : : :		
Db	1	AGCCTGCTTCTTCTACAACTGT 25		
RESULT 2				
ARI24527				
LOCUS	ARI24527	25 bp	DNA	linear
DEFINITION	Sequence 7 from patent US 6171861.			
ACCESSION	ARI24527			
VERSION	ARI24527.1	GI:14109888		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 25)			
AUTHORS	Hartley, J.L. and Brasch, M.A.			
TITLE	Recombinational cloning using engineered recombination sites			

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JOURNAL Patent: US 6171861-A 7 09-JAN-2001;
FEATURES
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  Best Local Similarity 68.0%; Pred. No. 37;
  Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASCCWGCTTTTTRTACWAASTKGW 25
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Db 1 AGCCTGCTTTTCTGTACAACTTGT 25
  |:::|||||:::|||||:::|||||:::|:
RESULT 3
AR124528 AR124528 25 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 8 from patent US 6171861.
ACCESSION AR124528
VERSION AR124528.1 GI:14109889
KEYWORDS
SOURCE
ORGANISM
  Unclassified.
  1 (bases 1 to 25)
  Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 8 09-JAN-2001;
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  Best Local Similarity 68.0%; Pred. No. 37;
  Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASCCWGCTTTTTRTACWAASTKGW 25
  |:::|||||:::|||||:::|||||:::|:
Db 1 ACCCAGCTTTCTGTACAACTTGT 25
  |:::|||||:::|||||:::|||||:::|:
RESULT 4
AR124551 AR124551 25 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 31 from patent US 6171861.
ACCESSION AR124551
VERSION AR124551.1 GI:14109912
KEYWORDS
SOURCE
ORGANISM
  Unclassified.
  1 (bases 1 to 25)
  Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 31 09-JAN-2001;
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  Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASCCWGCTTTTTRTACWAASTKGW 25
  |:::|||||:::|||||:::|||||:::|:
Db 1 ACCCAGCTTTCTGTACAACTTGT 25
  |:::|||||:::|||||:::|||||:::|:
RESULT 5
AR124552 AR124552 25 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 32 from patent US 6171861.
ACCESSION AR124552
VERSION AR124552.1 GI:14109913
KEYWORDS
SOURCE
ORGANISM
  Unclassified.
  1 (bases 1 to 25)
  Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 32 09-JAN-2001;
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  Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
AR124553 AR124553 25 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 33 from patent US 6171861.
ACCESSION AR124553
VERSION AR124553.1 GI:14109914
KEYWORDS
SOURCE
ORGANISM
  Unclassified.
  1 (bases 1 to 25)
  Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 33 09-JAN-2001;
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Qy 1 ASCCWGCTTTTTRTACWAASTKGW 25
  |:::|||||:::|||||:::|||||:::|:
Db 25 AGCCTGCTTTTATATACTACTTGA 1
  |:::|||||:::|||||:::|||||:::|:
RESULT 7
AR124554 AR124554 25 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 34 from patent US 6171861.
ACCESSION AR124554
VERSION AR124554.1 GI:14109915
KEYWORDS
SOURCE
ORGANISM
  Unclassified.
  1 (bases 1 to 25)
  Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 34 09-JAN-2001;
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  Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASCCGCTTTTTRTACWAATKGW 25
Db 25 AGCCTGCTTTCTGTACAACTTGT 1
RESULT 8
AR124555/c
LOCUS AR124555 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 35 from patent US 6171861.
ACCESSION AR124555
VERSION AR124555.1 GI:14109916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 25)
  Hartley,J.L. and Brasch,M.A.
  Recombinational cloning using engineered recombination sites
  TITLE
  JOURNAL
  PATENT: US 6171861-A 35 09-JAN-2001;
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  Best Local Similarity 68.0%; Pred. No. 37;
  Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASCCGCTTTTTRTACWAATKGW 25
Db 25 ACCCAGCTTTCTGTACAACTTGT 1
RESULT 9
AR163177
LOCUS AR163177 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 6 from patent US 6270969.
ACCESSION AR163177
VERSION AR163177.1 GI:16233685
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 25)
  Hartley,J.L. and Brasch,M.A.
  Recombinational cloning using engineered recombination sites
  TITLE
  JOURNAL
  PATENT: US 6270969-A 6 07-AUG-2001;
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Db 1 AGCCTGCTTTTCTGTACAACTTGT 25
RESULT 10
AR163178
LOCUS AR163178 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 7 from patent US 6270969.
ACCESSION AR163178
VERSION AR163178.1 GI:16233686
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 25)
  Hartley,J.L. and Brasch,M.A.
  Recombinational cloning using engineered recombination sites
  TITLE
  JOURNAL
  PATENT: US 6270969-A 7 07-AUG-2001;
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ORIGIN
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Qy 1 ASCCGCTTTTTRTACWAATKGW 25
Db 1 AGCCTGCTTTTCTGTACAACTTGT 25
RESULT 11
AR163179
LOCUS AR163179 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6270969.
ACCESSION AR163179
VERSION AR163179.1 GI:16233687
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 25)
  Hartley,J.L. and Brasch,M.A.
  Recombinational cloning using engineered recombination sites
  TITLE
  JOURNAL
  PATENT: US 6270969-A 8 07-AUG-2001;
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  Best Local Similarity 68.0%; Pred. No. 37;
  Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASCCGCTTTTTRTACWAATKGW 25
Db 1 ACCCAGCTTTCTGTACAACTTGT 25
RESULT 12
AR163202
LOCUS AR163202 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 31 from patent US 6270969.
ACCESSION AR163202
VERSION AR163202.1 GI:16233722
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 25)
  Hartley,J.L. and Brasch,M.A.
  Recombinational cloning using engineered recombination sites
  TITLE
  JOURNAL
  PATENT: US 6270969-A 31 07-AUG-2001;
  FEATURES
    Location/Qualifiers
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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.8	87.2	25	2	AAT48216
2	21.8	87.2	25	2	AAT48215
3	21.8	87.2	25	2	AAT48217
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5	21.8	87.2	25	2	AAT48217
6	21.8	87.2	25	2	AAT48217
7	21.8	87.2	25	2	AAT48217
8	21.8	87.2	25	2	AAT48217
9	21.8	87.2	25	2	AAT48217
10	21.8	87.2	25	2	AAT48217
11	21.8	87.2	25	2	AAT48217
12	21.8	87.2	25	2	AAT48217
13	21.8	87.2	25	2	AAT48217
14	21.8	87.2	25	2	AAT48217
15	21.8	87.2	25	2	AAT48217
16	21.8	87.2	25	2	AAT48217
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18	21.8	87.2	25	2	AAT48217
19	21.8	87.2	25	2	AAT48217
20	21.8	87.2	25	2	AAT48217
21	21.8	87.2	25	2	AAT48217

ALIGNMENTS

RESULT 1  
AAT48216  
ID AAT48216 standard; DNA; 25 BP.  
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AC AAT48216;  
XX  
DT 20-OCT-1997 (first entry)  
XX  
DB attB2 core region.  
XX  
KW att recombination site; core region; mutation; enhance; recombination;  
KW vector; subcloning; regulation; exchange; ss.  
XX Synthetic.  
OS  
PN WO9640724-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 07-JUN-1996; 96WO-US010082.  
XX  
PR 07-JUN-1995; 95US-00486139.  
XX (LIFE-) LIFE TECHNOLOGIES INC.  
XX Hartley JL, Brasch MA;  
XX WPI, 1997-065168/06.  
XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
XX using recombinant proteins and engineered recombination sites in vitro or  
XX in vivo.  
XX Claim 14; Page 55; 106pp; English.  
XX AAT48210-25 are att recombination site core region DNA sequences. The  
XX core region has at least one engineered mutation that enhances  
XX recombination in vitro in the formation of a Cointegrate or Product DNA.  
XX These core regions can be incorporated into novel vector donor DNA  
XX molecules. The nucleic acids, vectors and methods of the invention are  
XX used to obtain chimeric nucleic acid using recombination proteins and  
XX engineered recombination sites in vitro or in vivo. The improved  
XX specificity, speed and yields of the invention facilitates DNA or RNA  
XX subcloning, regulation or exchange useful for any related purpose, e.g.



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XX WO9921977-A1.
XX
XX
XX PD 06-MAY-1999.
XX
XX PF 26-OCT-1998; 98WO-US022589.
XX
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX
XX DR WPI; 1999-303011/25.
XX
XX PT New nucleic acid cloning methods.
XX
XX PS Disclosure; Page 176; 185pp; English.
XX
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
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XX SQ Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 2; Length 25;
Best Local Similarity 68.0%; Pred. No. 5.4;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTATTACWAASTKGW 25
Db 1 AGCCTGCTTTTATTACTAAGTTGA 25

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AAX78940
ID AAX78940 standard; DNA; 25 BP.
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XX AC AAX78940;
XX
XX DT 17-AUG-1999 (first entry)
XX
XX DE Oligonucleotide #6 for recombination and cloning method.
XX
XX KW Cloning; donor; recombination site; vector; chimeric; ss.
XX
XX OS Synthetic.
XX
XX PN WO9921977-A1.
XX
XX PD 06-MAY-1999.
XX
XX PF 26-OCT-1998; 98WO-US022589.
XX
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX
XX DR WPI; 1999-303011/25.
XX
XX PT New nucleic acid cloning methods.
XX
XX PS Disclosure; Page 176; 185pp; English.
XX
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
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XX SQ Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 2; Length 25;
Best Local Similarity 68.0%; Pred. No. 5.4;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTATTACWAASTKGW 25
Db 1 AGCCTGCTTTTATTACTAAGTTGA 25

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ID AAX78942 standard; DNA; 25 BP.
XX
XX AC AAX78942;
XX
XX DT 17-AUG-1999 (first entry)
XX
XX DE Oligonucleotide #8 for recombination and cloning method.
XX
XX KW Cloning; donor; recombination site; vector; chimeric; ss.
XX
XX OS Synthetic.
XX
XX PN WO9921977-A1.
XX
XX PD 06-MAY-1999.
XX
XX PF 26-OCT-1998; 98WO-US022589.
XX
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX
XX DR WPI; 1999-303011/25.
XX
XX PT New nucleic acid cloning methods.
XX
XX PS Disclosure; Page 160; 185pp; English.
XX
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
XX
XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 2; Length 25;
Best Local Similarity 68.0%; Pred. No. 5.4;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTATTACWAASTKGW 25
Db 1 AGCCTGCTTTTATTACTAAGTTGT 25

RESULT 6
AAX78942
ID AAX78942 standard; DNA; 25 BP.
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XX AC AAX78942;
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XX DT 17-AUG-1999 (first entry)
XX
XX DE Oligonucleotide #8 for recombination and cloning method.
XX
XX KW Cloning; donor; recombination site; vector; chimeric; ss.
XX
XX OS Synthetic.
XX
XX PN WO9921977-A1.
XX
XX PD 06-MAY-1999.
XX
XX PF 26-OCT-1998; 98WO-US022589.
XX
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX
XX DR WPI; 1999-303011/25.
XX
XX PT New nucleic acid cloning methods.
XX
XX PS Disclosure; Page 160; 185pp; English.
XX
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
XX
XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

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```

XX 11-JAN-2001 (first entry)
DT Recombination site nucleotide sequence attB2.
DE
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS
XX WO200052027-A1.
PN
XX 08-SEP-2000.
PD
XX 02-MAR-2000; 2000WO-US005432.
PF
XX 02-MAR-1999; 99US-0122389P.
PR
XX 23-MAR-1999; 99US-0126049P.
PR
XX 28-MAY-1999; 99US-0136744P.
PR
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
PI WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.
XX
XX Claim 1; Fig 9; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX
SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 87.2%; Score 21.8; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 5.4;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ASCCGCTTTTTRTACWAATKGW 25
Db 1 ACCCAGCTTCTTGTCACAAAGTGT 25
RESULT 10
AAC55380/c
ID AAC55380 standard; DNA; 25 BP.
XX
XX AAC55380;
AC
XX

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DT 11-JAN-2001 (first entry)
DE Recombination site nucleotide sequence attB1.
DE
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS
XX WO200052027-A1.
PN
XX 08-SEP-2000.
PD
XX 02-MAR-2000; 2000WO-US005432.
PF
XX 02-MAR-1999; 99US-0122389P.
PR
XX 23-MAR-1999; 99US-0126049P.
PR
XX 28-MAY-1999; 99US-0136744P.
PR
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
PI WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.
XX
XX Claim 1; Fig 9; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX
SQ Sequence 25 BP; 11 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 87.2%; Score 21.8; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 5.4;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ASCCGCTTTTTRTACWAATKGW 25
Db 25 AGCCTGCTTTTGTGTCACAACTGT 1
RESULT 11
AAC55600/c
ID AAC55600 standard; DNA; 25 BP.
XX
XX AAC55600;
AC
XX
XX 11-JAN-2001 (first entry)

```









GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds  
(without alignments)  
494.978 Million cell updates/sec

Title: US-10-820-133-40

Perfect score: 25

Sequence: 1 ascwgctttrttacwaastkgw 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.8	87.2	25	3	US-09-233-493-6
2	21.8	87.2	25	3	US-09-233-493-7
3	21.8	87.2	25	3	US-09-233-493-8
4	21.8	87.2	25	3	US-09-233-493-31
5	21.8	87.2	25	3	US-09-233-493-32
6	21.8	87.2	25	3	US-09-233-493-33
7	21.8	87.2	25	3	US-09-233-493-34
8	21.8	87.2	25	3	US-09-233-493-35
9	21.8	87.2	25	3	US-09-005-476-6
10	21.8	87.2	25	3	US-09-005-476-7
11	21.8	87.2	25	3	US-09-005-476-8
12	21.8	87.2	25	3	US-09-005-476-31
13	21.8	87.2	25	3	US-09-005-476-32
14	21.8	87.2	25	3	US-09-005-476-33
15	21.8	87.2	25	3	US-09-005-476-34
16	21.8	87.2	25	3	US-09-005-476-35
17	21.8	87.2	25	3	US-09-233-492-6
18	21.8	87.2	25	3	US-09-233-492-7
19	21.8	87.2	25	3	US-09-233-492-8
20	21.8	87.2	25	3	US-09-233-492-31
21	21.8	87.2	25	3	US-09-233-492-32
22	21.8	87.2	25	3	US-09-233-492-33
23	21.8	87.2	25	3	US-09-233-492-34
24	21.8	87.2	25	3	US-09-233-492-35
25	21.8	87.2	25	3	US-09-296-280-6
26	21.8	87.2	25	3	US-09-296-280-7
27	21.8	87.2	25	3	US-09-296-280-8

28	21.8	87.2	25	3	US-09-296-280-40	Sequence 40, Appl
29	21.8	87.2	25	3	US-09-296-280-60	Sequence 60, Appl
30	21.8	87.2	25	4	US-09-498-074-6	Sequence 6, Appl
31	21.8	87.2	25	4	US-09-498-074-7	Sequence 7, Appl
32	21.8	87.2	25	4	US-09-498-074-8	Sequence 8, Appl
33	21.8	87.2	25	4	US-09-498-074-31	Sequence 31, Appl
34	21.8	87.2	25	4	US-09-498-074-32	Sequence 32, Appl
35	21.8	87.2	25	4	US-09-498-074-33	Sequence 33, Appl
36	21.8	87.2	25	4	US-09-498-074-34	Sequence 34, Appl
37	21.8	87.2	25	4	US-09-498-074-35	Sequence 35, Appl
38	21.8	87.2	25	4	US-09-498-074-6	Sequence 6, Appl
39	21.8	87.2	25	4	US-09-498-074-7	Sequence 7, Appl
40	21.8	87.2	25	4	US-09-498-074-8	Sequence 8, Appl
41	21.8	87.2	25	4	US-09-498-074-31	Sequence 31, Appl
42	21.8	87.2	25	4	US-09-498-074-32	Sequence 32, Appl
43	21.8	87.2	25	4	US-09-498-074-33	Sequence 33, Appl
44	21.8	87.2	25	4	US-09-498-074-34	Sequence 34, Appl
45	21.8	87.2	25	4	US-09-498-074-35	Sequence 35, Appl

#### ALIGNMENTS

RESULT 1  
US-09-233-493-6  
; Sequence 6, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
US-09-233-493-6







ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,476  
FILING DATE: herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
US-09-005-476-6

Query Match 87.2%; Score 21.8; DB 3; Length 25;  
Best Local Similarity 68.0%; Pred. No. 0.75;  
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTTRTACWAASTKGW 25  
Db 1 AGCCTGCTTTTGTGACAACTTGT 25

RESULT 10  
US-09-005-476-7  
; Sequence 7, Application US/09005476  
; Patent No. 6171861  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,476  
FILING DATE: herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA

US-09-005-476-7

Query Match 87.2%; Score 21.8; DB 3; Length 25;  
Best Local Similarity 68.0%; Pred. No. 0.75;  
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTTRTACWAASTKGW 25  
Db 1 AGCCTGCTTTTGTGACAACTTGT 25

RESULT 11  
US-09-005-476-8  
; Sequence 8, Application US/09005476  
; Patent No. 6171861  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,476  
FILING DATE: herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/663,002  
FILING DATE: 07-JUN-1996  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
US-09-005-476-8

Query Match 87.2%; Score 21.8; DB 3; Length 25;  
Best Local Similarity 68.0%; Pred. No. 0.75;  
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTTRTACWAASTKGW 25  
Db 1 ACCGAGCTTTTGTGACAACTTGT 25

RESULT 12  
US-09-005-476-31  
; Sequence 31, Application US/09005476  
; Patent No. 6171861  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

```
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-31

Query Match      87.2%; Score 21.8; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 0.75;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASCCGCTTTTTRTACWAASTKGW 25
Db      1 AGCGTCTTTTATACTACTTGA 25

RESULT 13
US-09-005-476-32/c
; Sequence 32, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-32

Query Match      87.2%; Score 21.8; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 0.75;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASCCGCTTTTTRTACWAASTKGW 25
Db      25 AGCGTCTTTTATACTACTTGA 1

RESULT 14
US-09-005-476-33/c
; Sequence 33, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-33

Query Match      87.2%; Score 21.8; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 0.75;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASCCGCTTTTTRTACWAASTKGW 25
Db      25 AGCGTCTTTTATACTACTTGT 1

RESULT 15
US-09-005-476-34/c
; Sequence 34, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
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Search completed: November 16, 2004, 10:22:31  
Job time : 35.9 secs

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1 AGCCTGCTTTTGTACAACTTGT 25

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RESULT 4
US-09-855-797A-6
; Sequence 6, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-6

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Best Local Similarity 68.0%; Pred. No. 3.8;
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**Dd**

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US-09-855-797A-7
; Sequence 7, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-7

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Query Match	87.2%;	Score 21.8;	DB 9;	Length 25;
Best Local Similarity	68.0%;	Pred. No. 3.8;		
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Db 1 AGCCTGCTTCTTCTGTACAACTTGT 25

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US-09-855-797A-8  
; Sequence 8, Application US/09855797A  
; Patent No. US20020094574A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850008  
; CURRENT APPLICATION NUMBER: US/09/855,797A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/296,281  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-855-797A-8

Query Match 87.2%; Score 21.8; DB 9; Length 25;  
Best Local Similarity 68.0%; Pred. No. 3.8;  
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACCCAGCTTCTTCTGTACAAAGTGGT 25

## RESULT 7

US-09-855-797A-40  
; Sequence 40, Application US/09855797A  
; Patent No. US20020094574A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850008  
; CURRENT APPLICATION NUMBER: US/09/855,797A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/296,281  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 40  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-855-797A-40

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Best Local Similarity 100.0%; Pred. No. 3.8;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 8

US-09-855-797A-60  
; Sequence 60, Application US/09855797A  
; Patent No. US20020094574A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850008  
; CURRENT APPLICATION NUMBER: US/09/855,797A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/296,281  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
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; OTHER INFORMATION: products  
US-09-855-797A-60

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Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 9

US-09-907-900-6  
; Sequence 6, Application US/09907900  
; Patent No. US20020172997A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,900  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-900-6

Query Match 87.2%; Score 21.8; DB 9; Length 25;  
Best Local Similarity 68.0%; Pred. No. 3.8;







GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds  
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Searched: 32822875 segs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	21.8	87.2	83	6	CB401650 OSTR197D3
5	21.8	87.2	87	7	CF652842 80-L02016
6	21.8	87.2	89	7	CF651862 19-L02052
7	21.8	87.2	89	7	CF652759 75-L02013
8	21.8	87.2	89	7	CF653076 94-L02036
9	21.8	87.2	93	7	CF652843 80-L02016
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17	21.8	87.2	95	7	CF652127 35-L02057
18	21.8	87.2	95	7	CF652128 35-L02057
19	21.8	87.2	95	7	CF652167 38-L02036
20	21.8	87.2	95	7	CF652261 44-L02036
21	21.8	87.2	95	7	CF652333 49-L02013
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24	21.8	87.2	95	7	CF652546 62-L02036

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29	21.8	87.2	95	7	CF652617 66-L02052
30	21.8	87.2	95	7	CF652673 69-L02058
31	21.8	87.2	95	7	CF652698
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33	21.8	87.2	95	7	CF652763 75-L02057
34	21.8	87.2	95	7	CF652837 79-L02057
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ACCESSION CF651937  
VERSION CF651937  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
REFERENCE 1 (bases 1 to 79)  
AUTHORS Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weishaar, B.  
TITLE Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana  
JOURNAL Genome Res. 13 (6), 1250-1257 (2003)  
MEDLINE 226833290  
PUBMED 12799357  
COMMENT Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
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JOURNAL	Genome Res.	13	(6)		1250-1257	(2003)
MEDLINE	22883290					
PUBMED	12799357					
COMMENT	Contact: Weisshaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weisshaa@mpiz-koeln.mpg.de Insert Length: 87 Std Error: 0.00 Plate: 1 row: P column: 19 Seq primer: SP6P; Location/Qualifiers 1..87 /organism="Arabidopsis thaliana" /mol_type="mRNA" /ecotype="Ws-0" /db_xref="GABI:939445" /db_xref="taxon:3702" /clone="MP12p2001P191Q" /tissue_type="root" /lab_host="E. coli TOP10" /clone_lib="MPIZ-ADIS-066" /vector="pcmvSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from Arabidopsis thaliana, accession Wassilwskija-0; roots from three weeks old plants grown on MS-plates at 26M-OC with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGGCTTC-Sprime-cDNA-polyA-CC-NotI-T7; GATEWAY compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection'; PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."					
ORIGIN	Query Match	87.2%		Score	21.8;	DB 7; Length 87;
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VERSION	CF651862.1					
KEYWORDS	EST					
SOURCE	Arabidopsis thaliana (thale cress)					
ORGANISM	Arabidopsis thaliana					
REFERENCE	1 (bases 1 to 89)					
AUTHORS	Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.					
TITLE	Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana					
JOURNAL	Genome Res.	13	(6)		1250-1257	(2003)
MEDLINE	22883290					
PUBMED	12799357					
COMMENT	Contact: Weisshaar B ADIS DNA core facility at MPIZ					
CB401650.1	GI:30743377					
EST.						
Caenorhabditis elegans						
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;						
Rhabditoidea; Rhabditidae; Peleoderinae; Caenorhabditis.						
1 (bases 1 to 83)						
Reboult,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhautte,J., Boulton,S., Endress,G.A., Jenna.S., Chevret,E., Papasotiropoulos,V., Tollas,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H., Doucette-Stamm,L., Hill,D.E. and Vidal,M.						
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression						
Nat. Genet. (2003) In press						
Contact: Vidal M						
Marc Vidal Laboratory						
Dana Farber Cancer Institute						
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA						
Tel: 617 632 5180						
Fax: 617 632 5739						
Email: Marc.Vidal@dfci.harvard.edu						
Sequence tag of gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu						
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LOCATION/Qualifiers						
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ORIGIN	Query Match	87.2%		Score	21.8;	DB 6; Length 83;
	Best Local Similarity	68.0%;		Pred. No.	53;	
	Matches	17;	Conservative	8;	Mismatches	0; Indels 0; Gaps 0;
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RESULT 5						
CF652842						
LOCUS						
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ACCESSION	CF652842					
VERSION	CF652842.1					
KEYWORDS	EST					
SOURCE	Arabidopsis thaliana (thale cress)					
ORGANISM	Arabidopsis thaliana					
REFERENCE	1 (bases 1 to 87)					
AUTHORS	Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.					
TITLE	Large-scale identification and analysis of genome					

Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weissaha@mpiz-koeln.mpg.de  
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 Location/Qualifiers

## FEATURES

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 Wassilewskija-0; roots from three weeks old plants grown  
 on MS-plates at 26M-OC with 16 hours light/day; library  
 was made at the Max-Planck-Institute for Plant Breeding  
 Research, Cologne, Germany; cloning sites Sali-NotI,  
 primer sites and orientation:  
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 compatible; Note: Sequencing granted in the context of the  
 GABI Arabidopsis Verbund I: Genetic Diversity,  
 'Establishment of high-efficiency SNP-based mapping tools  
 and development of methods for genome-wide mutation  
 detection' PI: Bernd Weisshaar Sequence submission managed  
 by RZPD/GABI-Primary database: http://gabi.rzpd.de This  
 clone is available from RZPD; contact RZPD (clone@rzpd.de)  
 for further information."

## ORIGIN

Query Match 87.2%; Score 21.8; DB 7; Length 89;  
 Best Local Similarity 68.0%; Pred. No. 54;  
 Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTCTTACWAASTKGW 25

Db 44 ACCCAGCTTTCTTGACAAAGTGGT 68

## RESULT 7

CF652759

LOCUS

DEFINITION 75-L020135w-066-001-E19-SP6P MP12-ADIS-066 Arabidopsis thaliana  
 cDNA clone MP12P2001E191Q 5-PRIME, mRNA sequence.

ACCESSION

CF652759

VERSION

CF652759.1

KEYWORDS

EST.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 89)

REFERENCE

AUTHORS

Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,  
 Mitchell-Olds,T. and Weisshaar,B.

TITLE

Large-scale identification and analysis of genome-wide  
 single-nucleotide polymorphisms for mapping in Arabidopsis thaliana

JOURNAL

MEDLINE

PUBMED

22683290

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP12

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissaha@mpiz-koeln.mpg.de

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 cDNA library from Arabidopsis thaliana, accession  
 Wassilewskija-0; roots from three weeks old plants grown  
 on MS-plates at 26M-OC with 16 hours light/day; library  
 was made at the Max-Planck-Institute for Plant Breeding  
 Research, Cologne, Germany; cloning sites Sali-NotI,  
 primer sites and orientation:  
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY  
 compatible; Note: Sequencing granted in the context of the  
 GABI Arabidopsis Verbund I: Genetic Diversity,  
 'Establishment of high-efficiency SNP-based mapping tools  
 and development of methods for genome-wide mutation  
 detection' PI: Bernd Weisshaar Sequence submission managed  
 by RZPD/GABI-Primary database: http://gabi.rzpd.de This  
 clone is available from RZPD; contact RZPD (clone@rzpd.de)  
 for further information."

## ORIGIN

Query Match 87.2%; Score 21.8; DB 7; Length 89;  
 Best Local Similarity 68.0%; Pred. No. 54;  
 Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTCTTACWAASTKGW 25

Db 44 ACCCAGCTTTCTTGACAAAGTGGT 68

## RESULT 8

CF653076

LOCUS

DEFINITION 94-L020361-066-002-L23-SP6P MP12-ADIS-066 Arabidopsis thaliana cDNA  
 clone MP12P2001L232Q 5-PRIME, mRNA sequence.

ACCESSION

CF653076

VERSION

CF653076.1

KEYWORDS

EST.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 89)

REFERENCE

AUTHORS

Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,  
 Mitchell-Olds,T. and Weisshaar,B.

TITLE

Large-scale identification and analysis of genome-wide  
 single-nucleotide polymorphisms for mapping in Arabidopsis thaliana

JOURNAL

MEDLINE

PUBMED

22683290

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP12

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissaha@mpiz-koeln.mpg.de

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 93)
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.
Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
22683290
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 95)
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.
Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
22683290
PUBMED
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Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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ORIGIN
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Best Local Similarity 68.0%; Pred. No. 54;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

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VERSION
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SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 95)
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.
Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
22683290
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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ORIGIN
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RESULT 9
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VERSION
KEYWORDS
SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 93)
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.
Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
22683290
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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Wasilewskija-0; roots from three weeks old plants grown on MS-plates at 26W-OC with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCAGCGTCGCG-3prime-cDNA-polyA-CC-NotI-T7; GATEWAY compatible; CCAGCGTCGCG-3prime-NotI; Genetic Diversity, GABI Arabidopsis Verbund I; Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection; PI: Bernd Weisshaar Sequence submission managed by RZPP/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information."

## ORIGIN

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            Research, Cologne, Germany; cloning sites SalI-NotI,
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SP6-Sall-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection', PI: Bernd Weissnahr Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information."

## ORIGIN

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was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites SalI-NotI,
primer sites and orientation:
S6-SalI-CCACGCTCG-Prime-cDNA-polyA-CC-NotI-T7; GATEWAY
compatible; Note: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity,
'establishment of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation

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9	23	92.0	25	6	AR493786	AR493786	Sequence
10	23	92.0	25	6	AX269138	AX269138	Sequence
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TITLE	Compositions and methods for tissue specific gene regulation				
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Job time : 709.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds  
(without alignments)  
782.095 Million cell updates/sec

Title: US-10-820-133-41

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Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
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- 10: Geneseqn2003cs:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

## RESULT 1

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ID AAT48221 standard; DNA; 25 BP.

XX AC AAT48221;

DT 20-OCT-1997 (first entry)

XX attL1 core region.

XX att recombination site; core region; mutation; enhance; recombination;  
vector; subcloning; regulation; exchange; ss.

OS Synthetic.

PN WO9640724-A1.

PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
using recombinant proteins and engineered recombination sites in vitro or  
in vivo.

XX Claim 14; Page 56; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The  
core region has at least one engineered mutation that enhances  
recombination in vitro in the formation of a Cointegrate or Product DNA.  
These core regions can be incorporated into novel vector donor DNA  
molecules. The nucleic acids, vectors and methods of the invention are  
used to obtain chimeric nucleic acid using recombination proteins and  
engineered recombination sites in vitro or in vivo. The improved  
specificity, speed and yields of the invention facilitates DNA or RNA  
subcloning, regulation or exchange useful for any related purpose, e.g.

ABQ82124 Core sequ  
ABT16632 Artificia  
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ADA38174 DNA of a  
ADA38173 DNA of a  
ADA38175 DNA of a  
Aad60569 Core regi  
Aad60570 Core regi  
Acc44663 Recombina  
Acc44662 Recombina  
Acc44661 Recombina  
Adl93429 Recombina  
Adl93427 Recombina  
Adl93428 Recombina  
Aas06176 Phage-lam  
Aas06180 Phage-lam



```
XX PN WO9921977-A1.
XX PD 06-MAY-1999.
XX PF 26-OCT-1998; 98WO-US022589.
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX DR WPI; 1999-303011/25.
XX PT New nucleic acid cloning methods.
XX PS Disclosure; Page 162; 185pp; English.
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
XX SQ Sequence 25 BP; 5 A; 5 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 92.0%; Score 23; DB 2; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCWGCTTTTTRTACWAAAGTTGG 25
Db 1 AGCCTGCTTCTCTGTACAAAGTTGG 25

RESULT 5
AAX78975
ID AAX78975 standard; DNA; 25 BP.
XX AC AAX78975;
XX DT 17-AUG-1999 (first entry)
XX DE Oligonucleotide #41 for recombination and cloning method.
XX KW Cloning; donor; recombination site; vector; chimeric; ss.
XX OS Synthetic.
XX PN WO9921977-A1.
XX PD 06-MAY-1999.
XX PF 26-OCT-1998; 98WO-US022589.
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX DR WPI; 1999-303011/25.
XX PT New nucleic acid cloning methods.
XX PS Disclosure; Page 162; 185pp; English.
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
XX SQ Sequence 25 BP; 5 A; 5 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 92.0%; Score 23; DB 2; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCWGCTTTTTRTACWAAAGTTGG 25
Db 1 AGCCTGCTTCTCTGTACAAAGTTGG 25

RESULT 6
AAX78948
ID AAX78948 standard; DNA; 25 BP.
XX AC AAX78948;
XX DT 17-AUG-1999 (first entry)
XX DE Oligonucleotide #14 for recombination and cloning method.
XX KW Cloning; donor; recombination site; vector; chimeric; ss.
XX OS Synthetic.
XX PN WO9921977-A1.
XX PD 06-MAY-1999.
XX PF 26-OCT-1998; 98WO-US022589.
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX DR WPI; 1999-303011/25.
XX PT New nucleic acid cloning methods.
XX PS Disclosure; Page 162; 185pp; English.
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
XX SQ Sequence 25 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 5 Other;
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```

RESULT 9
AAC87879
ID AAC87879 standard; DNA; 25 BP.
XX
AC AAC87879;
XX
DT 02-MAR-2001 (first entry)
DE Escherichia coli core region recombinant site attL3 SEQ ID NO:14.
XX
KW Core region; recombination site; cloning; chimeric DNA; characteristic;
XX mutation; att site; lox site; ss.
XX
OS Escherichia coli.
XX
PN US6143557-A.
XX
PD 07-NOV-2000.
XX
PF 20-JAN-1999; 99US-002333493.
XX
PR 07-JUN-1995; 95US-00486139.
XX
PR 07-JUN-1996; 96US-00663002.
XX
PR 12-JAN-1998; 98US-00005476.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Hartley JL;
XX
DR WPI; 2001-049004/06.
XX
PT Isolated nucleic acid molecules comprising a DNA segment having two
PT engineered recombination sites, derived from att or lox, which flank a
PT selectable marker and comprise a core region having an engineered
PT mutation.
XX
PS Claim 1; Col 18; 73pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first
CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the above
CC mentioned nucleic acid; and (4) cells comprising the above mentioned
CC nucleic acids or (IV). The nucleic acids are used in engineering a core
CC region of a given recombination site to provide mutative sites suitable
CC for subcloning reactions. The use of nucleic acids for obtaining
CC engineered recombination in vitro or in vivo makes the methods for DNA or
CC RNA subcloning, highly specific, rapid, and less labour intensive
XX
SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 92.0%; Score 23; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASCCGCTTTTTRTACAAAGTTGG 25
Db 1 ACCCAGCTTCTTGTACAAAGTTGG 25
RESULT 10
AAC87877
ID AAC87877 standard; DNA; 25 BP.
XX
AC AAC87877;
XX

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DT 02-MAR-2001 (first entry)
DE Escherichia coli core region recombinant site attL1 SEQ ID NO:12.
XX
KW Core region; recombination site; cloning; chimeric DNA; characteristic;
XX mutation; att site; lox site; ss.
XX
OS Escherichia coli.
XX
PN US6143557-A.
XX
PD 07-NOV-2000.
XX
PF 20-JAN-1999; 99US-002333493.
XX
PR 07-JUN-1995; 95US-00486139.
XX
PR 07-JUN-1996; 96US-00663002.
XX
PR 12-JAN-1998; 98US-00005476.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Hartley JL;
XX
DR WPI; 2001-049004/06.
XX
PT Isolated nucleic acid molecules comprising a DNA segment having two
PT engineered recombination sites, derived from att or lox, which flank a
PT selectable marker and comprise a core region having an engineered
PT mutation.
XX
PS Claim 1; Col 18; 73pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first
CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the above
CC mentioned nucleic acid; and (4) cells comprising the above mentioned
CC nucleic acids or (IV). The nucleic acids are used in engineering a core
CC region of a given recombination site to provide mutative sites suitable
CC for subcloning reactions. The use of nucleic acids for obtaining
CC engineered recombination in vitro or in vivo makes the methods for DNA or
CC RNA subcloning, highly specific, rapid, and less labour intensive
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;
Query Match 92.0%; Score 23; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASCCGCTTTTTRTACAAAGTTGG 25
Db 1 AGCCTGCTTTTGTACAAAGTTGG 25
RESULT 11
AAF55748
ID AAF55748 standard; DNA; 25 BP.
XX
AC AAF55748;
XX
DT 12-APR-2001 (first entry)
XX
DE Recombination site attL3.
XX
KW Recombination site; cloning; att; ss.
XX
OS Unidentified.

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XX PN US6171861-B1.
XX PD 09-JAN-2001.
XX PF 12-JAN-1998; 98US-00005476.
XX PR 07-JUN-1995; 95US-00486139.
XX PR 07-JUN-1996; 96US-00663002.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA;
XX DR WPI; 2001-136877/14.
XX PT In vitro cloning of nucleic acid involves mixing vectors comprising
XX PT recombination sites and/or nucleic acid, incubating mixture to produce
XX PT chimeric molecule, contacting hosts with mixture and selecting host.
XX PS Claim 25; Col 46; 73pp; English.
XX CC The present invention relates to a method for in vitro cloning of a
XX CC nucleic acid of interest. The method involves mixing in vitro two vectors
XX CC each comprising at least one recombination site and the nucleic acid of
XX CC interest; incubating the mixture in the presence of at least one
XX CC recombination protein to result in recombination of the recombination
XX CC sites, leading to production of a chimeric nucleic acid molecule
XX CC comprising the nucleic acid of interest; contacting hosts with the
XX CC mixture; and selecting for a host comprising the chimeric nucleic acid
XX CC molecule, and selecting against a host comprising the vectors comprising
XX CC the second vector, to clone the nucleic acid. The present sequence is a
XX CC recombination site, which may be used in the method of the present
XX CC invention
XX SQ Sequence 25 BP; 5 A; 5 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 92.0%; Score 23; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCCGCTTTTTRTACWAAGTTGG 25
Db 1 AGCTGCTTTCTGTACAAAGTTGG 25

RESULT 13
AAF55746
ID AAF55746 standard; DNA; 25 BP.
XX AC AAF55746;
XX DT 12-APR-2001 (first entry)
XX DE Recombination site attL1.
XX KW Recombination site; cloning; att; ss.
XX OS Unidentified.
XX PN US6171861-B1.
XX PD 09-JAN-2001.
XX PF 12-JAN-1998; 98US-00005476.
XX PR 07-JUN-1995; 95US-00486139.
XX PR 07-JUN-1996; 96US-00663002.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA;
XX DR WPI; 2001-136877/14.
XX PT In vitro cloning of nucleic acid involves mixing vectors comprising
XX PT recombination sites and/or nucleic acid, incubating mixture to produce
XX PT chimeric molecule, contacting hosts with mixture and selecting host.
XX PS Claim 25; Col 46; 73pp; English.
XX CC The present invention relates to a method for in vitro cloning of a
XX CC nucleic acid of interest. The method involves mixing in vitro two vectors
XX CC each comprising at least one recombination site and the nucleic acid of
XX CC interest; incubating the mixture in the presence of at least one
XX CC recombination protein to result in recombination of the recombination
XX CC sites, leading to production of a chimeric nucleic acid molecule
XX CC comprising the nucleic acid of interest; contacting hosts with the
XX CC mixture; and selecting for a host comprising the chimeric nucleic acid
XX CC molecule, and selecting against a host comprising the vectors comprising
XX CC the second vector, to clone the nucleic acid. The present sequence is a
XX CC recombination site, which may be used in the method of the present
XX CC invention
XX SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 92.0%; Score 23; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCCGCTTTTTRTACWAAGTTGG 25
Db 1 ACCGAGCTTTCTGTACAAAGTTGG 25

RESULT 12
AAF55747
ID AAF55747 standard; DNA; 25 BP.
XX AC AAF55747;
XX DT 12-APR-2001 (first entry)
XX DE Recombination site attL2.
XX KW Recombination site; cloning; att; ss.
XX OS Unidentified.
XX PN US6171861-B1.
XX PD 09-JAN-2001.
XX PF 12-JAN-1998; 98US-00005476.
XX PR 07-JUN-1995; 95US-00486139.
XX PR 07-JUN-1996; 96US-00663002.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA;
XX DR WPI; 2001-136877/14.
XX PT In vitro cloning of nucleic acid involves mixing vectors comprising
XX PT recombination sites and/or nucleic acid, incubating mixture to produce
XX PT chimeric molecule, contacting hosts with mixture and selecting host.
XX PS Claim 25; Col 46; 73pp; English.
XX CC The present invention relates to a method for in vitro cloning of a
XX CC nucleic acid of interest. The method involves mixing in vitro two vectors
XX CC each comprising at least one recombination site and the nucleic acid of
XX CC interest; incubating the mixture in the presence of at least one
XX CC recombination protein to result in recombination of the recombination
XX CC sites, leading to production of a chimeric nucleic acid molecule
XX CC comprising the nucleic acid of interest; contacting hosts with the
XX CC mixture; and selecting for a host comprising the chimeric nucleic acid
XX CC molecule, and selecting against a host comprising the vectors comprising
XX CC the second vector, to clone the nucleic acid. The present sequence is a
XX CC recombination site, which may be used in the method of the present
XX CC invention
XX SQ Sequence 25 BP; 5 A; 5 C; 6 G; 9 T; 0 U; 0 Other;
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds  
(without alignments)  
494.978 Million cell updates/sec

Title: US-10-820-133-41

Perfect score: 25

Sequence: 1 ascwggtttrttacwaagtgg 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

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- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	92.0	25	3	US-09-233-493-12
2	23	92.0	25	3	US-09-233-493-13
3	23	92.0	25	3	US-09-233-493-14
4	23	92.0	25	3	US-09-005-476-12
5	23	92.0	25	3	US-09-005-476-13
6	23	92.0	25	3	US-09-005-476-14
7	23	92.0	25	3	US-09-233-492-12
8	23	92.0	25	3	US-09-233-492-13
9	23	92.0	25	3	US-09-233-492-14
10	23	92.0	25	3	US-09-296-280-12
11	23	92.0	25	3	US-09-296-280-13
12	23	92.0	25	3	US-09-296-280-14
13	23	92.0	25	3	US-09-296-280-41
14	23	92.0	25	4	US-09-498-074-12
15	23	92.0	25	4	US-09-498-074-13
16	23	92.0	25	4	US-09-498-074-14
17	23	92.0	25	4	US-09-498-074-12
18	23	92.0	25	4	US-09-498-074-13
19	23	92.0	25	4	US-09-498-074-14
20	23	92.0	25	5	PCT-US96-10082A-12
21	23	92.0	25	5	PCT-US96-10082A-13
22	23	92.0	25	5	PCT-US96-10082A-14
23	23	92.0	228	4	US-09-107-532A-667
24	23	92.0	2408	1	US-08-486-013-69
25	23	92.0	2408	2	US-08-482-279-69
26	23	92.0	2408	2	US-08-342-268-69
27	23	92.0	2408	3	US-09-015-968-69

28	23	92.0	2408	3	US-09-397-386-69	Sequence 69, Appl
29	23	92.0	3484	3	US-09-308-090-1	Sequence 1, Appl
30	23	92.0	3484	4	US-09-380-090A-1	Sequence 1, Appl
31	23	92.0	3757	2	US-09-016-366A-13	Sequence 13, Appl
32	23	92.0	3757	2	US-08-978-404B-19	Sequence 19, Appl
c 33	23	92.0	5349	3	US-09-068-101-7	Sequence 7, Appl
c 34	23	92.0	5349	4	US-09-970-921-7	Sequence 7, Appl
c 35	23	92.0	5611	3	US-09-068-101-10	Sequence 10, Appl
c 36	23	92.0	5611	4	US-09-970-921-10	Sequence 10, Appl
37	21.2	84.8	25	3	US-09-296-280-40	Sequence 40, Appl
38	20.4	81.6	25	3	US-09-233-493-6	Sequence 6, Appl
39	20.4	81.6	25	3	US-09-233-493-7	Sequence 7, Appl
40	20.4	81.6	25	3	US-09-233-493-8	Sequence 8, Appl
41	20.4	81.6	25	3	US-09-233-493-11	Sequence 11, Appl
42	20.4	81.6	25	3	US-09-233-493-15	Sequence 15, Appl
43	20.4	81.6	25	3	US-09-233-493-16	Sequence 16, Appl
44	20.4	81.6	25	3	US-09-233-493-31	Sequence 31, Appl
c 45	20.4	81.6	25	3	US-09-233-493-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1  
US-09-233-493-12  
; Sequence 12, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
US-09-233-493-12



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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005.476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-12

Query Match          92.0%; Score 23; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTTRTACWAAGTTGG 25
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Db 1 AGCCTGCTTTTCTGTACAAAGTTGG 25

RESULT 5
US-09-005-476-13
; Sequence 13, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005.476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-13

Query Match          92.0%; Score 23; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCCTGCTTTTCTGTACAAAGTTGG 25

US-09-005-476-14
; Sequence 14, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005.476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-14

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Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACCCAGCTTTCTGTACAAAGTTGG 25

RESULT 6
US-09-005-476-14
; Sequence 14, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005.476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-14

Query Match          92.0%; Score 23; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACCCAGCTTTCTGTACAAAGTTGG 25

RESULT 7
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; Sequence 12, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005.476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-13

Query Match          92.0%; Score 23; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTTRTACWAAGTTGG 25
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Db 1 ACCCAGCTTTCTGTACAAAGTTGG 25
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
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FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-14
Query Match 92.0%; Score 23; DB 3; Le
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 20; Conservative 5; Mismatches 0;
1 ASCCGCTTCTTCTTACWAAGTTGG 25

```

**Oy**

1 ASCCWGCTTTTYYTRACWAAGTTGG 25  
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**Dp**

1 AGCCTGTTTTCTGTACAAGTTGG 25

US-09-296-280-14  
: Sequence 14. Application US/09296280

TYPE: DNA  
ORGANISM: Unknown

US-09-296-280-14

OTHER INFORMATION: products  
US-09-296-280-14

Best Local Similarity 80.08; Pred. No. 0.22;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 1 ACCCAGCTTTCITGTACAAAGTTGG 25

RESULT 13  
US-09-296-280-41  
; Sequence 41, Application US/09296280  
; Patent No. 6277608  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.

```

, APPLICANT: Brasch, Michael A.
, APPLICANT: Temple, Gary F.
, APPLICANT: Fox, Donna K.
, TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
, TITLE OF INVENTION: Recombination Sites
, FILE REFERENCE: 0942.285007
, CURRENT APPLICATION NUMBER: US/09/296,280
, CURRENT FILING DATE: 1999-04-22
, EARLIER APPLICATION NUMBER: US 09/177,387
, EARLIER FILING DATE: 1998-10-23
, EARLIER APPLICATION NUMBER: US 60/065,930

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TYPE: DNA  
ORGANISM: Unknown

US-09-296-280-41





Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	23	92.0	25	9	US-09-855-797A-12	Sequence 12, Appl
2	23	92.0	25	9	US-09-855-797A-13	Sequence 13, Appl
3	23	92.0	25	9	US-09-855-797A-14	Sequence 14, Appl
4	23	92.0	25	9	US-09-855-797A-41	Sequence 41, Appl
5	23	92.0	25	9	US-09-822-634-9	Sequence 9, Appl
6	23	92.0	25	9	US-09-822-634-10	Sequence 10, Appl
7	23	92.0	25	9	US-09-822-634-11	Sequence 11, Appl
8	23	92.0	25	9	US-09-907-900-12	Sequence 12, Appl
9	23	92.0	25	9	US-09-907-900-13	Sequence 13, Appl
10	23	92.0	25	9	US-09-907-900-14	Sequence 14, Appl
11	23	92.0	25	9	US-09-907-900-41	Sequence 41, Appl
12	23	92.0	25	9	US-09-907-719-12	Sequence 12, Appl

Query Match 92.0%; Score 23; DB 9; Length 25;  
Best Local Similarity 80.0%; Pred. No. 1.3;  
Matches 20: Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Query Match 92.0%; Score 23; DB 9; Length 25;  
Best Local Similarity 80.0%; Pred. No. 1.3;  
Matches 20: Conservative 5; Mismatches 0; Indels 0; Gaps 0;

## RESULT 8

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RESULT 8
US-09-907-900-12
; Sequence 12, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-12

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Query Match 92.0%; Score 23; DB 9; Length 25;  
Best Local Similarity 80.0%; Pred. No. 1.3;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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		:   :   :   :   :   :   :   :	
pb	1	AGCGTGCTTTTTGTACAAAAGTTGG	25

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RESULT 9
US-09-907-900-13
; Sequence 13, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; US-09-907-900-13

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Query Match 92.0%; Score 23; DB 9; Length 25;  
Best Local Similarity 80.0%; Pred No. 1.3;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

**Qy**

1 ASCCWGCTTTTYYTRTACWAAGTTGG 25  
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**pB**

1 AGCGTGTTTTCTTGTACAAAATTGG 25

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Query Match      92.0%; Score 23; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match      92.0% Score 23; DB 9; Length 25;
Best Local Similarity 80.0%; Pred No. 1,3;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0
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Job time : 314.1 secs

RESULT 14  
US-09-907-719-14  
; Sequence 14, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-719-14

Query Match	92.0%;	Score 23;	DB 9;	Length 25;
Best Local Similarity	80.0%;	Pred. No. 1.3;		
Matches	20;	Conservative	5;	Mismatches 0; Indels 0; Gaps 0;

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RESULT 15  
US-09-907-719-41  
; Sequence 41, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41  
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; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-719-41

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Best Local Similarity	100.0%;	Pred. No. 1.3;		
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Db	1	ASCCWGCCTTTTTRTACWAAGTTGG	25

Search completed: November 16, 2004, 11:15:00

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds  
(without alignments)  
594.643 Million cell updates/sec

Title: US-10-820-133-41  
Perfect score: 25  
Sequence: 1 ascwgtttttrttacwaagtgg 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_g881:\*
- 9: gb\_g882:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	23	92.0	92	CB402537	CB402537 OSTF214C1
C 4	23	92.0	94	CB402408	CB402408 OSTF212B6
C 5	23	92.0	95	CB400591	CB400591 OSTF179E7
C 6	23	92.0	95	CB401751	CB401751 OSTF198G7
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C 12	23	92.0	100	CB398991	CB398991 OSTR213C8
C 13	23	92.0	100	CB400512	CB400512 OSTF177G3
C 14	23	92.0	102	CB392040	CB392040 OSTF162H1
C 15	23	92.0	102	CB399013	CB399013 OSTR213H5
C 16	23	92.0	103	CB396276	CB396276 OSTF169D1
C 17	23	92.0	103	CB401874	CB401874 OSTR202B1
C 18	23	92.0	104	CB396275	CB396275 OSTF169C5
C 19	23	92.0	106	CB396817	CB396817 OSTR179E7
C 20	23	92.0	107	CB388456	CB388456 OSTF099E7
C 21	23	92.0	108	CB398919	CB398919 OSTR212B7
C 22	23	92.0	111	CB394444	CB394444 OSTR137H4
C 23	23	92.0	111	CB395510	CB395510 OSTR158A1
C 24	23	92.0	112	CB396297	CB396297 OSTR170A1

C 25	23	92.0	112	6	CB397516	CB397516 OSTR191C6
C 26	23	92.0	112	6	CB398322	CB398322 OSTR202B1
C 27	23	92.0	118	6	CB396745	CB396745 OSTR177G3
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C 29	23	92.0	120	6	CB400382	CB400382 OSTF175B7
C 30	23	92.0	121	6	CB392422	CB392422 OSTF099E7
C 31	23	92.0	121	6	CB399813	CB399813 OSTF163C2
C 32	23	92.0	126	6	CB400130	CB400130 OSTF169C5
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C 34	23	92.0	128	6	CB401884	CB401884 OSTF202C5
C 35	23	92.0	129	6	CB401218	CB401218 OSTF191C6
C 36	23	92.0	141	6	CB388073	CB388073 OSTF091E1
C 37	23	92.0	190	6	CB396819	CB396819 OSTR179F1
C 38	23	92.0	225	6	CB397320	CB397320 OSTR186E2
C 39	23	92.0	227	6	CB398923	CB398923 OSTR212B6
C 40	23	92.0	227	6	CB398923	CB398923 OSTR212B6
C 41	23	92.0	247	6	CB401020	CB401020 OSTF186E2
C 42	23	92.0	247	6	CB401020	CB401020 OSTF186E2
C 43	23	92.0	262	6	CB395877	CB395877 OSTR163A3
C 44	23	92.0	262	6	CB395877	CB395877 OSTR163A3
C 45	23	92.0	263	6	CB395890	CB395890 OSTR163C2

ALIGNMENTS

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DEFINITION OSTF167D8\_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.  
ACCESSION CB400039  
VERSION CB400039.1 GI:30741766  
KEYWORDS EST.  
SOURCE Caenorhabditis elegans  
ORGANISM Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 87)  
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,  
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,  
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,  
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,  
Tollia,P., Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,  
Douce-Stamm,L., Hill,D.E. and Vidal,M.  
C. elegans ORFome version 1.1: experimental verification of the  
genome annotation and resource for proteome-scale protein  
expression  
JOURNAL Nat. Genet. (2003) In press  
COMMENT Contact: Vidal M  
Marc Vidal Laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 859, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739  
Email: Marc.Vidal@dfci.harvard.edu  
Sequence tag of Gateway entry clones. The primers used were  
designed on the predicted protein encoding ORF. C. elegans ORFome  
cloning project : Contact david\_hill@dfci.harvard.edu or  
marc\_vidal@dfci.harvard.edu  
POLY(A)=No..

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Db          33 ACCGAGCTTCTTGTCACAAAGTTGG 9

RESULT 14
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DEFINITION OSTRF16ZH10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB392040
VERSION    CB392040.1 GI:30733750
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 102)
AUTHORS   Rebol,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
            Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
            Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
            Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
            Tollias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
            Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE     C. elegans ORFeome version 1.1: experimental verification of the
            genome annotation and resource for proteome-scale protein
            expression
JOURNAL   Nat. Genet. (2003) In press
COMMENT   Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc.Vidal@dfci.harvard.edu
            Sequence tag of Gateway entry clones. The primers used were
            designed on the predicted protein encoding ORF. C. elegans ORPeome
            cloning project : Contact david_hill@dfci.harvard.edu or
            marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES             Location/Qualifiers
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ORIGIN
Query Match       92.0%; Score 23; DB 6; Length 102;
Best Local Similarity 80.0%; Pred. No. 16;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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DB      49 AGCCGTGCTTTTTTGTACAAAGTTGG 25

Search completed: November 16, 2004, 10:16:36
Job time : 1533 secs


Db          33 ACCGAGCTTCTTGTCACAAAGTTGG 9

RESULT 14
CB392040/c LOCUS      102 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTRF16ZH10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB392040
VERSION    CB392040.1 GI:30733750
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 102)
AUTHORS   Rebol,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
            Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
            Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
            Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
            Tollias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
            Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE     C. elegans ORFeome version 1.1: experimental verification of the
            genome annotation and resource for proteome-scale protein
            expression
JOURNAL   Nat. Genet. (2003) In press
COMMENT   Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc.Vidal@dfci.harvard.edu
            Sequence tag of Gateway entry clones. The primers used were
            designed on the predicted protein encoding ORF. C. elegans ORPeome
            cloning project : Contact david_hill@dfci.harvard.edu or
            marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="whole animal"
                     /dev_stage="mixed stage"
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                        RNA isolated from both hermaphrodite and male N2 worms of
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                        subsequent generation of cDNAs by poly(A) priming. The
                        cDNAs were cloned into pPC86"

ORIGIN
Query Match       92.0%; Score 23; DB 6; Length 102;
Best Local Similarity 80.0%; Pred. No. 16;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 ASCCGCTTTTTRTACWAAGTTGG 25
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DB      38 ACCCAGCTTCTTGTCACAAAGTTGG 14

RESULT 15
CB399013/c LOCUS      102 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR213H5_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB399013
VERSION    CB399013.1 GI:30740740
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida;

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:43 ; Search time 708.5 Seconds  
(without alignments)  
1668.656 Million cell updates/sec

Title: US-10-820-133-42  
Perfect score: 25  
Sequence: 1 gttcagcttcttttacwaaastkgw 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
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12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	22.6	90.4	25	6	AR124530 Sequence
3	22.6	90.4	25	6	AR163180 Sequence
4	22.6	90.4	25	6	AR163181 Sequence
5	22.6	90.4	25	6	AR493781 Sequence
6	22.6	90.4	25	6	AR493782 Sequence
7	22.6	90.4	25	6	AX491648 Sequence
8	22.6	90.4	25	6	AX491649 Sequence
9	22.6	90.4	25	6	AX498619 Sequence
10	22.6	90.4	25	6	AX498620 Sequence
11	22.6	90.4	25	6	AX787509 Sequence
12	22.6	90.4	25	6	AX787513 Sequence
13	22.6	90.4	25	6	BD131335 Recombina
14	22.6	90.4	25	6	BD131336 Recombina
15	22.6	90.4	25	6	BD131337 Recombina
16	22.6	90.4	25	6	BD131368 Recombina
17	22.6	90.4	27	6	AX787505 Sequence
18	22.6	90.4	35	6	AX684688 Sequence
19	22.6	90.4	37	6	CQ758822 Sequence

C 20	22.6	90.4	43	6	BD263259	Compositi
C 21	22.6	90.4	43	6	BD263260	Compositi
C 22	22.6	90.4	82	6	BD263456	Compositi
C 23	22.6	90.4	87	6	BD263465	Compositi
C 24	22.6	90.4	95	6	BD263452	Compositi
C 25	22.6	90.4	100	6	CQ758821	Sequence
C 26	22.6	90.4	102	6	BD263430	Compositi
C 27	22.6	90.4	102	6	BD263454	Compositi
C 28	22.6	90.4	102	6	BD263457	Compositi
C 29	22.6	90.4	102	6	BD263459	Compositi
C 30	22.6	90.4	102	6	BD263460	Compositi
C 31	22.6	90.4	102	6	BD263461	Compositi
C 32	22.6	90.4	102	6	BD263462	Compositi
C 33	22.6	90.4	120	6	BD263427	Compositi
C 34	22.6	90.4	125	6	BD263227	Compositi
C 35	22.6	90.4	125	6	AX787501	Sequence
C 36	22.6	90.4	135	6	BD263228	Compositi
C 37	22.6	90.4	153	6	BD263445	Compositi
C 38	22.6	90.4	153	6	BD263447	Compositi
C 39	22.6	90.4	153	6	BD263458	Compositi
C 40	22.6	90.4	204	6	BD263433	Compositi
C 41	22.6	90.4	204	6	BD263434	Compositi
C 42	22.6	90.4	204	6	BD263437	Compositi
C 43	22.6	90.4	204	6	BD263440	Compositi
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C 45	22.6	90.4	255	6	BD263435	Compositi

#### ALIGNMENTS

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LOCUS AR124529 Sequence 9 from patent US 6171861. 25 bp DNA linear PAT 16-MAY-2001  
ACCESSION AR124529  
VERSION AR124529.1 GI:14109890  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley, U.L. and Brasch, M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: US 6171861-A 9 09-JAN-2001;  
FEATURES Location/Qualifiers  
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LOCUS AR124530 Sequence 10 from patent US 6171861. 25 bp DNA linear PAT 16-MAY-2001  
ACCESSION AR124530  
VERSION AR124530.1 GI:14109891  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley, U.L. and Brasch, M.A.  
TITLE Recombinational cloning using engineered recombination sites





[illegible]

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DEFINITION Sequence 30 from Patent WO03044207.
ACCESSION AX787513
VERSION AX787513.1 GI:32954587
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1
AUTHORS Nomura,N., Goshima,N., Kieu,Y. and Sono,S.
TITLE Method for the preparation of nucleic acids
JOURNAL Patent: WO 03044207-A 30 30-MAY-2003;
Industrial Science and Technology (JP)
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Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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sites.
ACCESSION BD131335
VERSION BD131335.1 GI:23226280
KEYWORDS JP 2002500861-A/9.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 9 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/9
PD 15-JAN-2002
PR 26-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DONNA K. FOX PC
C12N15/09,C12Q1/68,C12N15/00
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Key Location/Qualifiers
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VERSION BD131336.1 GI:23226281
KEYWORDS JP 2002500861-A/10.
SOURCE unidentified
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REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 10 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/10
PD 15-JAN-2002
PR 26-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DONNA K. FOX PC
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DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION BD131337
VERSION BD131337.1 GI:23226282
KEYWORDS JP 2002500861-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 11 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/11
PD 15-JAN-2002
PR 26-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DONNA K. FOX PC
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LOCUS
DEFINITION Recombinational cloning using nucleic acids having recombination
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ACCESSION BD131338
VERSION BD131338.1 GI:23226283
KEYWORDS JP 2002500861-A/12.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 12 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/12
PD 15-JAN-2002
PR 26-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DONNA K. FOX PC
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Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTCTGACAAAGTGGT 25  
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Db 1 GTTCAGCTTCTTCTGACAAAGTGGT 25  
|||

Search completed: November 16, 2004, 06:01:03  
Job time : 708.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds  
(without alignments)  
782.095 Million cell updates/sec

Title: US-10-820-133-42

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	22.6	90.4	25	2 AAT48219	Aat48219 attR2 cor
2	22.6	90.4	25	2 AAT48218	Aat48218 attR1 cor
3	22.6	90.4	25	2 AAX78944	Aax78944 Oligonucl
4	22.6	90.4	25	2 AAX78945	Aax78945 Oligonucl
5	22.6	90.4	25	2 AAX78976	Aax78976 Oligonucl
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8	22.6	90.4	25	2 AAS06185	Aas06185 Phage-lam
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11	22.6	90.4	25	4 AAF55744	Aaf55744 Recombina
12	22.6	90.4	25	4 AAF55743	Aaf55743 Recombina
13	22.6	90.4	25	4 AAD14437	Aad14437 Recombina
14	22.6	90.4	25	4 AAD14438	Aad14438 Recombina
15	22.6	90.4	25	6 ABQ82121	Abq82121 Core sequ
16	22.6	90.4	25	6 ABQ82122	Abq82122 Core sequ
17	22.6	90.4	25	8 ABT16628	Abt16628 Artificia
18	22.6	90.4	25	8 ABT16629	Abt16629 Artificia
19	22.6	90.4	25	9 ACD28284	Acd28284 Nucleic a
20	22.6	90.4	25	9 ACD28285	Acd28285 Nucleic a
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#### ALIGNMENTS

##### RESULT 1

AAT48219  
ID AAT48219 standard; DNA; 25 BP.

XX AC AAT48219;

XX DT 20-OCT-1997 (first entry)

XX DE attR2 core region.

XX att recombination site; core region; mutation; enhance; recombination;  
vector; subcloning; regulation; exchange; ss.

XX OS Synthetic.

XX PN WO9640724-A1.

XX PD 19-DEC-1996.

XX PP 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
using recombinant proteins and engineered recombination sites in vitro or  
in vivo.

XX Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The  
core region has at least one engineered mutation that enhances  
recombination in vitro in the formation of a co-integrate or product DNA.  
These core regions can be incorporated into novel vector donor DNA  
molecules. The nucleic acids, vectors and methods of the invention are  
used to obtain chimeric nucleic acid using recombination proteins and  
engineered recombination sites in vitro or in vivo. The improved  
specificity, speed and yields of the invention facilitates DNA or RNA  
subcloning, regulation or exchange useful for any related purpose, e.g.

22 22.6 90.4 25 9 ACD28484 Nucleic a  
23 22.6 90.4 25 9 ADA38171 DNA of a  
24 22.6 90.4 25 9 ADA38170 DNA of a  
25 22.6 90.4 25 10 AAD60567 Core regi  
26 22.6 90.4 25 10 AAD60566 Core regi  
27 22.6 90.4 25 10 ABZ58734 Att site  
28 22.6 90.4 25 10 ABZ58738 Att site  
29 22.6 90.4 25 10 ACC59582 Nucleic a  
30 22.6 90.4 25 10 ACC59578 Nucleic a  
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32 22.6 90.4 25 10 ACC44659 Recombina  
33 22.6 90.4 25 12 ADJ46352 Wild type  
34 22.6 90.4 25 12 ADJ46356 Wild type  
35 22.6 90.4 25 12 ADL93424 Recombina  
36 22.6 90.4 25 12 ADL93425 Recombina  
37 22.6 90.4 25 12 ADO06646 att recom  
38 22.6 90.4 25 12 ADO06650 att recom  
39 22.6 90.4 25 12 ADQ48458 Bacteriop  
40 22.6 90.4 25 12 ADQ48454 Bacteriop  
41 22.6 90.4 27 4 AAS06177 Phage-lam  
42 22.6 90.4 27 10 ABZ58730 Att site  
43 22.6 90.4 27 10 ACC59574 Nucleic a  
44 22.6 90.4 27 12 ADJ46348 Wild type  
45 22.6 90.4 27 12 ADO06642 att recom

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA  
 XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

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 Best Local Similarity 76.0%; Pred. No. 4.9;  
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 GTTCAGCTTTTCTGTACAACTTGT 25

## RESULT 2

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 ID AAT48218 standard; DNA; 25 BP.

XX AC AAT48218;

XX DT 20-OCT-1997 (first entry)

XX DE attR1 core region.

XX KW att recombination site; core region; mutation; enhance; recombination;  
 XX vector; subcloning; regulation; exchange; ss.

XX OS Synthetic.

XX PN WO9640724-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;

XX DR WPI; 1997-065168/06.

XX PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
 XX using recombinant proteins and engineered recombination sites in vitro or  
 XX in vivo.

XX PS Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The  
 CC core region has at least one engineered mutation that enhances  
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.  
 CC These core regions can be incorporated into novel vector donor DNA  
 CC molecules. The nucleic acids, vectors and methods of the invention are  
 CC used to obtain chimeric nucleic acid using recombination proteins and  
 CC engineered recombination sites in vitro or in vivo. The improved  
 CC specificity, speed and yields of the invention facilitates DNA or RNA  
 CC subcloning, regulation or exchange useful for any related purpose, e.g.  
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
 CC or modification of transcribed, replicated, isolated or genomic DNA or  
 CC RNA

XX SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 90.4%; Score 22.6; DB 2; Length 25;  
 Best Local Similarity 76.0%; Pred. No. 4.9;  
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAASTKGW 25

DB 1 GTTCAGCTTTTCTGTACAACTTGT 25

## RESULT 3

AAX78944

ID AAX78944 standard; DNA; 25 BP.

XX AC AAX78944;

XX DT 17-AUG-1999 (first entry)

XX DE Oligonucleotide #10 for recombination and cloning method.

XX KW Cloning; donor; recombination site; vector; chimeric; ss.

XX OS Synthetic.

XX PN WO9921977-A1.

XX PD 06-MAY-1999.

XX PF 26-OCT-1998; 98WO-US022589.

XX PR 24-OCT-1997; 97US-0065930P.

XX PR 23-OCT-1998; 98US-00177387.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;

XX DR WPI; 1999-303011/25.

XX PT New nucleic acid cloning methods.

XX PS Disclosure; Page 161; 185pp; English.

XX The invention relates to novel methods for cloning or subcloning one or  
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
 CC more desired nucleic acid segments flanked by at least 2 recombination  
 CC sites which do not recombine with each other; (2) one or more vector  
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
 CC not recombine with each other; and (3) one or more site-specific  
 CC recombination proteins; (b) incubating the combination to transfer one or  
 CC more of the desired segments into one or more of the VDMs, thereby can be  
 CC producing one or more desired product molecules (PMS). The methods can be  
 CC used for the efficient and specific recombination of NAM segments. They  
 CC can be used to generate chimeric DNA or RNA molecules that have the  
 CC desired characteristics and/or nucleic acid segments. The methods can  
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
 CC are used in the method of the invention

XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 90.4%; Score 22.6; DB 2; Length 25;  
 Best Local Similarity 76.0%; Pred. No. 4.9;  
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAASTKGW 25

DB 1 GTTCAGCTTTTCTGTACAACTTGT 25

## RESULT 4

AAX78945

ID AAX78945 standard; DNA; 25 BP.

XX AC AAX78945;

XX DT 17-AUG-1999 (first entry)

XX DE Oligonucleotide #11 for recombination and cloning method.

XX KW Cloning; donor; recombination site; vector; chimeric; ss.



CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
 CC not recombine with each other; and (3) one or more site-specific  
 CC recombination proteins; (b) incubating the combination to transfer one or  
 CC more of the desired segments into one or more of the VDMs, thereby  
 CC producing one or more desired product molecules (PwMs). The methods can be  
 CC used for the efficient and specific recombination of NAM segments. They  
 CC can be used to generate chimeric DNA or RNA molecules that have the  
 CC desired characteristics and/or nucleic acid segments. The methods can  
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
 CC are used in the method of the invention

XX SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 90.4%; Score 22.6; DB 2; Length 25;  
 Best Local Similarity 76.0%; Pred. No. 4.9;  
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25  
 Db 1 GTTCAGCTTTTGTACAAACTTGT 25

## RESULT 7

AAS06181  
 ID AAS06181 standard; DNA; 25 BP.

XX AC AAS06181;

XX DT 12-SEP-2001 (first entry)

XX DE Phage-lambda recombination site attR1.

XX KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;  
 XX KW lambda integrase; therapeutic; ss.

XX OS Bacteriophage lambda.

XX PN WO200142509-A1.

XX PD 14-JUN-2001.

XX PF 11-DEC-2000; 2000WO-US033546.

XX PR 10-DEC-1999; 99US-0169983P.

XX PR 09-MAR-2000; 2000US-0188020P.

XX PA (CHEO/) CHEO D.

XX PA (BRAS/) BRASCH M A.

XX PA (TEMP/) TEMPLE G F.

XX PA (HART/) HARTLEY J L.

XX PA (BYRD/) BYRD D R N.

XX PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

XX WPI; 2001-356174/37.

XX DR Producing hybrid nucleic acids, useful for expressing novel therapeutic  
 XX PT polypeptides, by mixing the same or different nucleic acids having one or  
 XX PT more recombination sites in the presence of recombination proteins, e.g.  
 XX PT Cre.

XX PS Disclosure; Fig 24A; 357pp; English.

XX SS AAS06174-AAS06322 represent Bacteriophage lambda att recombination site  
 CC nucleic acid sequences, and PCR primers of the invention. The att  
 CC sequences are recognised by the recombination protein lambda integrase  
 CC (Int). The invention is a new method of producing a population of hybrid  
 CC nucleic acids comprising mixing at least a first population of nucleic  
 CC acids comprising one or more recombination sites with at least one target  
 CC nucleic acid comprising one or more recombination sites and causing some  
 CC or all of the nucleic acids to recombine with all or some of the target  
 CC nucleic acids. The method is useful for producing a population of hybrid  
 CC nucleic acids which may be the same or different. The nucleic acids may

CC be used to express therapeutic proteins or peptides and they may also be  
 CC linked to create novel fusion proteins by expressing different sequences  
 CC linked to each other. The method allows simultaneous cloning of two or  
 CC more different nucleic acids

XX SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 90.4%; Score 22.6; DB 4; Length 25;  
 Best Local Similarity 76.0%; Pred. No. 4.9;  
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25  
 Db 1 GTTCAGCTTTTGTACAAACTTGT 25

## RESULT 8

AAS06185  
 ID AAS06185 standard; DNA; 25 BP.

XX AC AAS06185;

XX DT 12-SEP-2001 (first entry)

XX DE Phage-lambda recombination site attR2.

XX KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;  
 XX KW lambda integrase; therapeutic; ss.

XX OS Bacteriophage lambda.

XX PN WO200142509-A1.

XX PD 14-JUN-2001.

XX PF 11-DEC-2000; 2000WO-US033546.

XX PR 10-DEC-1999; 99US-0169983P.

XX PR 09-MAR-2000; 2000US-0188020P.

XX PA (CHEO/) CHEO D.

XX PA (BRAS/) BRASCH M A.

XX PA (TEMP/) TEMPLE G F.

XX PA (HART/) HARTLEY J L.

XX PA (BYRD/) BYRD D R N.

XX PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

XX WPI; 2001-356174/37.

XX DR Producing hybrid nucleic acids, useful for expressing novel therapeutic  
 XX PT polypeptides, by mixing the same or different nucleic acids having one or  
 XX PT more recombination sites in the presence of recombination proteins, e.g.  
 XX PT Cre.

XX PS Disclosure; Fig 24A; 357pp; English.

XX SS AAS06174-AAS06322 represent Bacteriophage lambda att recombination site  
 CC nucleic acid sequences, and PCR primers of the invention. The att  
 CC sequences are recognised by the recombination protein lambda integrase  
 CC (Int). The invention is a new method of producing a population of nucleic  
 CC acids comprising mixing at least a first population of nucleic  
 CC acids comprising one or more recombination sites with at least one target  
 CC nucleic acid comprising one or more recombination sites and causing some  
 CC or all of the nucleic acids to recombine with all or some of the target  
 CC nucleic acids. The method is useful for producing a population of hybrid  
 CC nucleic acids which may be the same or different. The nucleic acids may  
 CC be used to express therapeutic proteins or peptides and they may also be  
 CC used to create novel fusion proteins by expressing different sequences  
 CC linked to each other. The method allows simultaneous cloning of two or  
 CC more different nucleic acids

XX SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;



```

Query Match      90.4%; Score 22.6; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAATKGW 25
DB 1 GTTCAGCTTTTCTGTACAAAGTGT 25

RESULT 9
AAC87875
ID AAC87875 standard; DNA; 25 BP.
XX AAC87875;
XX
XX
XX 02-MAR-2001 (first entry)
XX Escherichia coli core region recombinant site attr2 SEQ ID NO:10.
XX Core region; recombination site; cloning; chimeric DNA; characteristic;
XX mutation; att site; lox site; ss.
XX Escherichia coli.
XX US6143557-A.
XX 07-NOV-2000.
XX 20-JAN-1999; 99US-00233493.
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX 12-JAN-1998; 98US-00005476.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Brasch MA, Hartley JL;
XX WPI; 2001-049004/06.
XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation.
XX Claim 1; Col 18; 73pp; English.
XX The present invention describes an isolated nucleic acid molecule (I)
XX comprising a first nucleic acid sequence having a defined sequence
XX (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
XX or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
XX are: (1) an isolated nucleic acid molecule (II) comprising a first
XX mutated recombination site that removes one or more stop codons from the
XX recombination site or avoids hairpin formation, the recombination site
XX being an att or lox site; (2) an isolated nucleic acid molecule (III)
XX comprising a first att recombination site comprising a mutation that
XX enhances recombination specificity; (3) vectors (IV) comprising the above
XX mentioned nucleic acids; and (4) cells comprising the above mentioned
XX nucleic acids or (IV). The nucleic acids are used in engineering a core
XX region of a given recombination site to provide mutative sites suitable
XX for subcloning reactions. The use of nucleic acids for obtaining
XX engineered recombination in vitro or in vivo makes the methods for DNA or
XX RNA subcloning, highly specific, rapid, and less labour intensive
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

Query Match      90.4%; Score 22.6; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAATKGW 25
DB 1 GTTCAGCTTTTCTGTACAAAGTGT 25

RESULT 11
AAF55744
ID AAF55744 standard; DNA; 25 BP.
XX

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DB 1 GTTCAGCTTTTCTGTACAAACTTGT 25

RESULT 10
AAC87874
ID AAC87874 standard; DNA; 25 BP.
XX AAC87874;
XX
XX 02-MAR-2001 (first entry)
XX Escherichia coli core region recombinant site attr1 SEQ ID NO:9.
XX Core region; recombination site; cloning; chimeric DNA; characteristic;
XX mutation; att site; lox site; ss.
XX Escherichia coli.
XX US6143557-A.
XX 07-NOV-2000.
XX 20-JAN-1999; 99US-00233493.
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX 12-JAN-1998; 98US-00005476.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Brasch MA, Hartley JL;
XX WPI; 2001-049004/06.
XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation.
XX Claim 1; Col 18; 73pp; English.
XX The present invention describes an isolated nucleic acid molecule (I)
XX comprising a first nucleic acid sequence having a defined sequence
XX (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
XX or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
XX are: (1) an isolated nucleic acid molecule (II) comprising a first
XX mutated recombination site that removes one or more stop codons from the
XX recombination site or avoids hairpin formation, the recombination site
XX being an att or lox site; (2) an isolated nucleic acid molecule (III)
XX comprising a first att recombination site comprising a mutation that
XX enhances recombination specificity; (3) vectors (IV) comprising the above
XX mentioned nucleic acids; and (4) cells comprising the above mentioned
XX nucleic acids or (IV). The nucleic acids are used in engineering a core
XX region of a given recombination site to provide mutative sites suitable
XX for subcloning reactions. The use of nucleic acids for obtaining
XX engineered recombination in vitro or in vivo makes the methods for DNA or
XX RNA subcloning, highly specific, rapid, and less labour intensive
XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match      90.4%; Score 22.6; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAATKGW 25
DB 1 GTTCAGCTTTTCTGTACAAACTTGT 25

RESULT 11
AAF55744
ID AAF55744 standard; DNA; 25 BP.
XX

```





acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents the core sequence of recombination site attB1 which is given in the exemplification of the present invention

Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

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Query Match          90.4%; Score 22.6; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTTCAGCTTTTYYTRTACWAASTKGW 25

Q3  
Db

Search completed: November 16, 2004, 04:02:49  
Job time : 167.8 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds  
(without alignments)  
494.978 Million cell updates/sec

Title: US-10-820-133-42  
Perfect score: 25  
Sequence: 1 gttcagcttcttctacwaaastkgw 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22.6	90.4	25	3	US-09-233-493-9
2	22.6	90.4	25	3	US-09-233-493-10
3	22.6	90.4	25	3	US-09-005-476-9
4	22.6	90.4	25	3	US-09-005-476-10
5	22.6	90.4	25	3	US-09-233-492-9
6	22.6	90.4	25	3	US-09-233-492-10
7	22.6	90.4	25	3	US-09-296-280-9
8	22.6	90.4	25	3	US-09-296-280-10
9	22.6	90.4	25	3	US-09-296-280-11
10	22.6	90.4	25	3	US-09-296-280-42
11	22.6	90.4	25	4	US-09-498-074-9
12	22.6	90.4	25	4	US-09-498-074-10
13	22.6	90.4	25	4	US-09-498-074-9
14	22.6	90.4	25	4	US-09-498-074-10
15	22.6	90.4	25	5	PCT-US96-10082A-9
16	22.6	90.4	25	5	PCT-US96-10082A-10
17	22	88.0	25	3	US-09-233-493-11
18	22	88.0	25	3	US-09-233-493-15
19	22	88.0	25	3	US-09-233-493-16
20	22	88.0	25	3	US-09-005-476-11
21	22	88.0	25	3	US-09-005-476-15
22	22	88.0	25	3	US-09-005-476-16
23	22	88.0	25	3	US-09-233-492-11
24	22	88.0	25	3	US-09-233-492-15
25	22	88.0	25	3	US-09-233-492-16
26	22	88.0	25	3	US-09-296-280-15
27	22	88.0	25	3	US-09-296-280-16

28	22	88.0	25	3	US-09-296-280-43	Sequence 43, Appl
29	22	88.0	25	4	US-09-498-074-11	Sequence 11, Appl
30	22	88.0	25	4	US-09-498-074-15	Sequence 15, Appl
31	22	88.0	25	4	US-09-498-074-16	Sequence 16, Appl
32	22	88.0	25	4	US-09-498-074-11	Sequence 11, Appl
33	22	88.0	25	4	US-09-498-074-15	Sequence 15, Appl
34	22	88.0	25	4	US-09-498-074-16	Sequence 16, Appl
35	22	88.0	25	5	PCT-US96-10082A-11	Sequence 11, Appl
36	22	88.0	25	5	PCT-US96-10082A-15	Sequence 15, Appl
37	22	88.0	25	5	PCT-US96-10082A-16	Sequence 16, Appl
38	22	88.0	201	1	US-08-021-667A-18	Sequence 18, Appl
39	22	88.0	201	1	US-08-410-544-18	Sequence 18, Appl
40	22	88.0	201	1	US-08-728-785A-18	Sequence 18, Appl
C 41	22	88.0	1763	4	US-09-244-805-57	Sequence 57, Appl
C 42	22	88.0	4909	3	US-08-556-978B-78	Sequence 78, Appl
C 43	22	88.0	6043	4	US-09-630-929-4	Sequence 4, Appl
44	22	88.0	7652	1	US-07-590-988A-1	Sequence 1, Appl
45	21.2	84.8	25	3	US-09-233-493-3	Sequence 3, Appl

#### ALIGNMENTS

RESULT 1  
US-09-233-493-9  
; Sequence 9, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
US-09-233-493-9



;; FILING DATE: 07-JUN-1996  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; MOLECULE TYPE: cdna  
US-09-005-476-10

Query Match 90.4%; Score 22.6; DB 3; Length 25;  
Best Local Similarity 76.0%; Pred. No. 0.96;  
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTGTG 25  
Db 1 GTTCAGCTTTTGTACAACTGTG 25

RESULT 5  
US-09-233-492-9  
; Sequence 9, Application US/09233492  
; Patent No. 6270969  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,492  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
US-09-233-492-9

Query Match 90.4%; Score 22.6; DB 3; Length 25;  
Best Local Similarity 76.0%; Pred. No. 0.96;  
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTTCAGCTTTTGTACAACTGTG 25

Db 1 GTTCAGCTTTTGTACAACTGTG 25

RESULT 6  
US-09-233-492-10  
; Sequence 10, Application US/09233492  
; Patent No. 6270969  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,492  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
US-09-233-492-10

Query Match 90.4%; Score 22.6; DB 3; Length 25;  
Best Local Similarity 76.0%; Pred. No. 0.96;  
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTGTG 25  
Db 1 GTTCAGCTTTTGTACAACTGTG 25

RESULT 7  
US-09-296-280-9  
; Sequence 9, Application US/09296280  
; Patent No. 6277608  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850007  
; CURRENT APPLICATION NUMBER: US/09/296,280  
; CURRENT FILING DATE: 1999-04-22

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; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-9

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
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Db 1 GTTCAGCTTTTGTGACAACTTGT 25

RESULT 8
US-09-296-280-10
; Sequence 10, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-10

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
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Db 1 GTTCAGCTTTTGTGACAACTTGT 25

RESULT 9
US-09-296-280-11
; Sequence 11, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-11

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
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Db 1 GTTCAGCTTTTGTGACAACTTGT 25

RESULT 10
US-09-296-280-42
; Sequence 42, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-42

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
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Db 1 GTTCAGCTTTTTRTACWAASTKGW 25

RESULT 11
US-09-498-074-9
; Sequence 9, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
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; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-11

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
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Db 1 GTTCAGCTTTTGTGACAACTTGT 25

RESULT 10
US-09-296-280-42
; Sequence 42, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-42

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
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Db 1 GTTCAGCTTTTTRTACWAASTKGW 25

RESULT 11
US-09-498-074-9
; Sequence 9, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
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;; TITLE OF INVENTION: Recombination Sites  
;; NUMBER OF SEQUENCES: 35  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
;; STREET: 1100 New York Ave., N. W. Suite 600  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005-3934  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/498,074  
;; FILING DATE: (Herewith)  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/005,476  
;; FILING DATE: 12-JAN-1998  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/663,002  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2540  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; MOLECULE TYPE: cDNA  
US-09-498-074-9

Query Match 90.4%; Score 22.6; DB 4; Length 25;  
Best Local Similarity 76.0%; Pred. NO. 0.96;  
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 GTTCAGCTTTTGTGACAACTTGT 25

RESULT 12  
US-09-498-074-10  
;; Sequence 10, Application US/09498074  
;; Patent No. 6534264  
;; GENERAL INFORMATION:  
;; APPLICANT: Hartley, James L.  
;; Brach, Michael A.  
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
;; RECOMBINATION SITES  
;; NUMBER OF SEQUENCES: 35  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
;; STREET: 1100 New York Ave., N. W. Suite 600  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005-3934  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/498,074  
;; FILING DATE: (Herewith)  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/005,476  
;; FILING DATE: 12-JAN-1998  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/663,002  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
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;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; MOLECULE TYPE: cDNA  
US-09-498-074-10  
  
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Best Local Similarity 76.0%; Pred. NO. 0.96;  
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 GTTCAGCTTTTGTGACAACTTGT 25  
  
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US-09-498-074-9  
;; Sequence 9, Application US/09498074  
;; Patent No. 6720140  
;; GENERAL INFORMATION:  
;; APPLICANT: Hartley, James L.  
;; Brach, Michael A.  
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
;; RECOMBINATION SITES  
;; NUMBER OF SEQUENCES: 35  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
;; STREET: 1100 New York Ave., N. W. Suite 600  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005-3934  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/498,074  
;; FILING DATE: 04-Feb-2000  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/005,476  
;; FILING DATE: 12-JAN-1998  
;; APPLICATION NUMBER: 08/663,002  
;; FILING DATE: 07-JUN-1995  
;; APPLICATION NUMBER: 08/486,139  
;; FILING DATE: 07-JUN-1995  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
430.015 Million cell updates/sec

Title: US-10-820-133-42

Perfect score: 25

Sequence: 1 gttcagctttttrttacwaaatkgw 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	22.6	90.4	25	9	US-09-855-797A-10
5	22.6	90.4	25	9	US-09-855-797A-11
6	22.6	90.4	25	9	US-09-855-797A-42
7	22.6	90.4	25	9	US-09-907-900-9
8	22.6	90.4	25	9	US-09-907-900-10
9	22.6	90.4	25	9	US-09-907-900-11
10	22.6	90.4	25	9	US-09-907-900-42
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12	22.6	90.4	25	9	US-09-907-719-10

13	22.6	90.4	25	9	US-09-907-719-11
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36	22.6	90.4	25	15	US-10-300-892-42
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42	22.6	90.4	25	16	US-10-680-316-42
43	22.6	90.4	25	17	US-10-815-730-9
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#### ALIGNMENTS

#### RESULT 1

US-09-732-914-8

Sequence 8, Application US/09732914

Patent No. US20020007051A1

GENERAL INFORMATION:

APPLICANT: Cheo, David

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Hartley, James L.

APPLICANT: Byrd, Devon R.N.

TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in File Reference: 0942.5010002

CURRENT APPLICATION NUMBER: US/09/732,914

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 60/169,983

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 60/188,020

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 140

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8

LENGTH: 25

TYPE: DNA

ORGANISM: attr1

US-09-732-914-8

Query Match 90.4%; Score 22.6; DB 9; Length 25;

Best Local Similarity 76.0%; Pred. No. 2.9;

Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTTACWAAATKGW 25

DB 1 GTTCAGCTTTTTRTTACWAAATKGW 25

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RESULT 4
US-09-855-797A-10
; Sequence 10, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-10

Query Match          90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0

Qy      1  GTTCAGCTTTTTRTACWAASTKGW 25
Db      1  GTTCAGCTTTCTGTACAACTGTT 25

RESULT 5
US-09-855-797A-11
; Sequence 11, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-11

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Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25  
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RESULT 10  
US-09-907-900-42  
; Sequence 42, Application US/09907900  
; Patent No. US20020172997A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,900  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-900-42

Query Match 90.4%; Score 22.6; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTTTRTACWAASTKGW 25

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US-09-907-719-9  
; Sequence 9, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-719-9

Query Match 90.4%; Score 22.6; DB 9; Length 25;  
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Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12  
US-09-907-719-10  
; Sequence 10, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-719-10

Query Match 90.4%; Score 22.6; DB 9; Length 25;  
Best Local Similarity 76.0%; Pred. No. 2.9;  
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13  
US-09-907-719-11  
; Sequence 11, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-719-11

Query Match 90.4%; Score 22.6; DB 9; Length 25;  
Best Local Similarity 76.0%; Pred. No. 2.9;  
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25  
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Db      1 GTTCAGCTTCTTGTACAAAGTGCT 25

RESULT 14
US-09-907-719-42
; Sequence 42, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
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; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-42

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Best Local Similarity 100.0%; Pred. NO. 2.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 9, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-432-085-9

Query Match      90.4%; Score 22.6; DB 10; Length 25;
Best Local Similarity 76.0%; Pred. NO. 2.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GTTCAGCTTCTTGTACAAAGTGCT 25

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
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(without alignments)  
594.643 Million cell updates/sec

Title: US-10-820-133-42  
Perfect score: 25  
Sequence: 1 gttcagctttttttacwaaatkgw 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsel:\*  
9: gb\_gsel2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	22.6	90.4	708	8 AQ990869	AQ990869 Rfc01706
C 2	22.6	90.4	770	8 AQ991774	AQ991774 Rfc02039F
C 3	22.6	90.4	791	8 AQ991791	AQ991791 Rfc02368F
C 4	22	88.0	206	5 BQ156416	BQ156416 NF092F021
C 5	22	88.0	299	5 BV115594	BV115594 BV115594
C 6	22	88.0	306	5 BP757615	BP757615 BP757615
C 7	22	88.0	374	5 BP754432	BP754432 BP754432
C 8	22	88.0	401	5 BP754410	BP754410 BP754410
C 9	22	88.0	409	5 BP754552	BP754552 BP754552
C 10	22	88.0	422	5 BP754464	BP754464 BP754464
C 11	22	88.0	423	5 BP754551	BP754551 BP754551
C 12	22	88.0	430	5 BP754589	BP754589 BP754589
C 13	22	88.0	432	5 BP754563	BP754563 BP754563
C 14	22	88.0	443	5 BP754508	BP754508 BP754508
C 15	22	88.0	443	5 BP754571	BP754571 BP754571
C 16	22	88.0	449	5 BP754440	BP754440 BP754440
C 17	22	88.0	472	5 BQ157398	BQ157398 NF104D071
C 18	22	88.0	473	5 BQ156404	BQ156404 NF032E031
C 19	22	88.0	482	5 BP754592	BP754592 BP754592
C 20	22	88.0	483	5 BP757892	BP757892 BP757892
C 21	22	88.0	486	5 BP754503	BP754503 BP754503
C 22	22	88.0	489	5 BP754581	BP754581 BP754581
C 23	22	88.0	546	5 BP754439	BP754439 BP754439
C 24	22	88.0	567	5 BP754491	BP754491 BP754491

C 25	22	88.0	597	4 BI422679	BI422679 EST513345
C 26	22	88.0	645	5 BP754484	BP754484 BP754484
C 27	22	88.0	671	5 BP754388	BP754388 BP754388
C 28	22	88.0	672	5 BP754535	BP754535 BP754535
C 29	22	88.0	672	8 AQ990864	AQ990864 Rfc01701
C 30	22	88.0	674	5 BP754519	BP754519 BP754519
C 31	22	88.0	689	5 BP754572	BP754572 BP754572
C 32	22	88.0	695	8 AQ991039	AQ991039 Rfc01894
C 33	22	88.0	712	8 AQ990809	AQ990809 Rfc01638
C 34	22	88.0	731	5 BP758121	BP758121 BP758121
C 35	22	88.0	743	8 AQ990346	AQ990346 Rfc01106
C 36	22	88.0	753	8 AQ990861	AQ990861 Rfc01698
C 37	22	88.0	764	8 AQ990110	AQ990110 Rfc00827
C 38	22	88.0	769	8 AQ990470	AQ990470 Rfc01245
C 39	22	88.0	808	8 AQ990388	AQ990388 Rfc01153
C 40	21.6	86.4	756	8 AQ991732	AQ991732 Rfc00380F
C 41	21.4	85.6	821	9 CL672759	CL672759 PRI017d A
C 42	21.4	85.6	875	9 CL688994	CL688994 PRI0150a
C 43	21	84.0	395	8 AQ991303	AQ991303 Rfc02205-
C 44	21	84.0	664	8 AQ991011	AQ991011 Rfc01864
C 45	21	84.0	719	8 AQ991352	AQ991352 Rfc02270

ALIGNMENTS

RESULT 1  
AQ990869/c  
LOCUS  
DEFINITION  
708 bp DNA linear GSS 14-AUG-2000  
Rfc01706 Photorhabdus luminescens strain W14 M13 library  
Photorhabdus luminescens genomic clone PLG01706, genomic survey  
sequence.  
ACCESSION  
AQ990869  
VERSION  
AQ990869.1 GI:9649463  
KEYWORDS  
GSS.  
SOURCE  
Photorhabdus luminescens  
ORGANISM  
Photorhabdus luminescens  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Photorhabdus.  
REFERENCE  
1 (bases 1 to 708)  
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,  
Daborn, P.J., Bowen, D. and Blattner, F.R.  
A genomic sample sequence of the entomopathogenic bacterium  
Photorhabdus luminescens W14: potential implications for virulence  
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)  
20378633  
10919786  
Contact: ffrench-Constant RH  
Department of Biology and Biochemistry  
University of Bath  
South Building, Bath BA2 7AY, UK  
Tel: (44) 1225 826621  
Fax: (44) 1225 826779  
Email: bsarfb@bath.ac.uk  
This is one of 2,122 random reads from the M13 library. For  
annotation of identified clones (BLASTX, BLASTN and mapping to E.  
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic  
Acids Res.  
Seq primer: M13 Forward  
Class: shotgun.  
Location/Qualifiers  
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kb) and then cloned into M13 Janus."

FEATURES  
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ORIGIN

Query Match 90.4%; Score 22.6; DB 8; Length 708;  
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Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25  
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 Db 348 GTTCAGCTTTTATACTAAGTGA 324

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 AQ991774/c  
 LOCUS  
 DEFINITION Rfc02039F Photorhabdus luminescens strain W14 M13 library  
 Photorhabdus luminescens genomic clone PLG02039F, genomic survey  
 sequence.

ACCESSION AQ991774  
 VERSION AQ991774.1 GI:9650368  
 KEYWORDS GSS.  
 SOURCE Photorhabdus luminescens  
 ORGANISM Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 770)  
 AUTHORS ffrrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,  
 Daborn,P.J., Bowen,D. and Blattner,F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium  
 Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE 20378633  
 PUBMED 10919786

COMMENT Contact: ffrrench-Constant RH  
 Department of Biology and Biochemistry  
 University of Bath  
 South Building, Bath BA2 7AY, UK

Tel: (44) 1225 826621  
 Fax: (44) 1225 826779

Email: bssrfc@bath.ac.uk  
 This is one of a selected subset of flipped clones from the M13  
 library. For annotation of identified clones (BLASTX, BLASTN and  
 mapping to E. coli K12 genome) please see ffrrench-Constant et al.

Seq primer: M13 Reverse  
 Class: shotgun.

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RESULT 3  
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 LOCUS  
 DEFINITION Rfc02368F Photorhabdus luminescens strain W14 M13 library  
 Photorhabdus luminescens genomic clone PLG02368F, genomic survey  
 sequence.

ACCESSION AQ991791  
 VERSION AQ991791.1 GI:9650385  
 KEYWORDS GSS.  
 SOURCE Photorhabdus luminescens  
 ORGANISM Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 791)  
 AUTHORS ffrrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,  
 Daborn,P.J., Bowen,D. and Blattner,F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium  
 Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE 20378633  
 PUBMED 10919786

COMMENT Contact: ffrrench-Constant RH  
 Department of Biology and Biochemistry  
 University of Bath  
 South Building, Bath BA2 7AY, UK

Tel: (44) 1225 826621  
 Fax: (44) 1225 826779

Email: bssrfc@bath.ac.uk  
 This is one of a selected subset of flipped clones from the M13  
 library. For annotation of identified clones (BLASTX, BLASTN and  
 mapping to E. coli K12 genome) please see ffrrench-Constant et al.

Seq primer: M13 Reverse  
 Class: shotgun.

FEATURES  
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 /dev\_stage="primary phase variant"  
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 /note="Genomic DNA from strain W14 was size selected (1-2  
 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 90.4%; Score 22.6; DB 8; Length 791;  
 Best Local Similarity 76.0%; Pred. No. 44;  
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25  
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 Db 56 GTTCAGCTTTTATACTAAGTGA 32

RESULT 4

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 LOCUS  
 DEFINITION NF092F021R1F1027 Irradiated Medicago truncatula cDNA clone  
 NF092F021R 5', mRNA sequence.

ACCESSION BQ156416  
 VERSION BQ156416  
 KEYWORDS EST.  
 SOURCE Medicago truncatula (barrel medic)  
 ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.  
 1 (bases 1 to 206)

REFERENCE 1 (bases 1 to 206)  
 AUTHORS Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
 Flores,H.R., Inman,J.I., Weller,J.W. and May,G.D.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula irradiated library  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: May GD  
 Plant Biology Division

The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 224 6650  
 Fax: 580 224 6692  
 Email: gdmay@noble.org  
 Insert Length: 206 Std Error: 0.00  
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 Location/Qualifiers  
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#### FEATURES

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 /tissue\_type="seedlings"  
 /dev\_stage="seedling"  
 /clone\_lib="Irradiated"  
 /note="Vector: Lambda Zap; Seedlings were exposed either to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m<sup>2</sup> UV irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. cDNA was prepared from polyA<sup>+</sup> enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

#### ORIGIN

Query Match 88.0%; Score 22; DB 5; Length 206;  
 Best Local Similarity 79.2%; Pred No. 68;  
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAATK 24

Db 167 GTTCAGCTTTTATCTAAGTTG 144

#### RESULT 5

BY115594  
 LOCUS  
 DEFINITION  
 musculus cDNA clone L430040C03 5', mRNA sequence.  
 BY115594.1 GI:26226695

#### VERSION

#### KEYWORDS

#### SOURCE

Mus musculus (house mouse)

#### ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 299)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bratt, D., Brusci, V., Chotha, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konggaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Akakawa, T., Fukuda, S., Hara, A., Haseizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

#### TITLE

JOURNAL  
 MEDLINE  
 PUBMED  
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AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 409)
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
JOURNAL pancreatic islets and its application to microarray
COMMENT unpublished (2004)
Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
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VERSION BP754464.1 GI:50074354
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 422)
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
JOURNAL pancreatic islets and its application to microarray
COMMENT unpublished (2004)
Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
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mRNA sequence.
ACCESSION BP754551
VERSION BP754551.1 GI:50074441
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 423)
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
JOURNAL pancreatic islets and its application to microarray
COMMENT unpublished (2004)
Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
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DEFINITION  BP754571 mouse (C57BL/6) pancreatic islet library with
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ACCESSION   BP754571
VERSION     BP754571.1   GI:50074461
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 443)
AUTHORS     Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
            Takeda,J., Ohara,O. and Seino,S.
TITLE       Construction of a multi-functional cDNA library specific for mouse
            pancreatic islets and its application to microarray
JOURNAL     Unpublished (2004)
COMMENT     Contact: Susumu Seino
            Division of Cellular and Molecular Medicine
            Kobe University Graduate School of Medicine
            7-5-1 Kusunoki-cho, Chuo-Ku, Kobe, Hyogo 650-0017, Japan
            Tel: 81-78-382-5360
            Fax: 81-78-382-5370
            Email: seino@med.kobe-u.ac.jp.
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
1668.656 Million cell updates/sec

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Sequence: 1 gttcagctttttrtacwaagtgg 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_ats.\*  
12: gb\_ay.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	23.8	95.2	25	6	ARI24535 Sequence
3	23.8	95.2	25	6	ARI24536 Sequence
4	23.8	95.2	25	6	ARI163182 Sequence
5	23.8	95.2	25	6	ARI163186 Sequence
6	23.8	95.2	25	6	ARI163187 Sequence
7	23.8	95.2	25	6	ARI163187 Sequence
8	23.8	95.2	25	6	ARI493783 Sequence
9	23.8	95.2	25	6	ARI493787 Sequence
10	23.8	95.2	25	6	ARI493788 Sequence
11	23.8	95.2	25	6	AX269137 Sequence
12	23.8	95.2	25	6	AX491650 Sequence
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27	23.8	95.2	233	6	BD263225 Compositi
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#### ALIGNMENTS

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ACCESSION ARI24531  
VERSION ARI24531.1 GI:14109892  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites  
JOURNAL Patent: US 6171861-A 11 09-JAN-2001;  
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ACCESSION ARI24535  
VERSION ARI24535.1 GI:14109896  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hartley,J.L. and Brasch,M.A.  
TITLE Recombinational cloning using engineered recombination sites

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JOURNAL Patent: US 6171861-A 15 09-JAN-2001;
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ACCESSION AR124536
VERSION AR124536.1 GI:14109897
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 16 09-JAN-2001;
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ACCESSION AR163182
VERSION AR163182.1 GI:16233692
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 11 07-AUG-2001;
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DEFINITION Sequence 15 from patent US 6270969.
ACCESSION AR163186
VERSION AR163186.1 GI:16233698
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 15 07-AUG-2001;
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DEFINITION Sequence 16 from patent US 6270969.
ACCESSION AR163187
VERSION AR163187.1 GI:16233699
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 16 07-AUG-2001;
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DEFINITION Sequence 11 from patent US 6720140.
ACCESSION AR493783
VERSION AR493783.1 GI:47266202
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 11 13-APR-2004;
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ACCESSION AR493787
VERSION AR493787.1 GI:47266210
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (Bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 15 13-APR-2004;
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ACCESSION AR493788
VERSION AR493788.1 GI:47266212
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (Bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 16 13-APR-2004;
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Db 1 GTTCAGCTTTCTGTACAAAGTTGG 25
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RESULT 10
LOCUS AX269137 25 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 8 from Patent WO0174861.
ACCESSION AX269137
VERSION AX269137.1 GI:16542057
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
  1
AUTHORS Ville,R.G., Harrington,K., Murphy,S. and Bateman,A.
TITLE Compositions and methods for tissue specific gene regulation
JOURNAL therapy: WO 0174861-A 8 11-OCT-2001;
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RESULT 11
LOCUS AX491650 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 11 from Patent EP1227147.
ACCESSION AX491650
VERSION AX491650.1 GI:22324158
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
  1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 11 31-JUL-2002;
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RESULT 12
LOCUS AX491654 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 15 from Patent EP1227147.
ACCESSION AX491654
VERSION AX491654.1 GI:22324162
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
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unclassified.
1
REFERENCE
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 15 31-JUL-2002;
INVITROGEN CORPORATION (US)
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Db 1 GTTCAGCTTTTGTGACAAAGTTGG 25

RESULT 15
AX498625
LOCUS AX498625 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 15 from Patent EP1229113.
ACCESSION AX498625
VERSION AX498625.1 GI:23343422
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 15 07-AUG-2002;
INVITROGEN CORPORATION (US)
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Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
AX498621
LOCUS AX498621 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 11 from Patent EP1229113.
ACCESSION AX498621
VERSION AX498621.1 GI:23343418
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 11 07-AUG-2002;
INVITROGEN CORPORATION (US)
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Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
AX491655
LOCUS AX491655 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 16 from Patent EP1227147.
ACCESSION AX491655
VERSION AX491655.1 GI:22324163
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 16 31-JUL-2002;
INVITROGEN CORPORATION (US)
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Best Local Similarity 88.0%; Pred. No. 19;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
|||||:|:|:|:|:|:|
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RESULT 13
AX491655
LOCUS AX491655 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 16 from Patent EP1227147.
ACCESSION AX491655
VERSION AX491655.1 GI:22324163
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 16 31-JUL-2002;
INVITROGEN CORPORATION (US)
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Best Local Similarity 88.0%; Pred. No. 19;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
|||||:|:|:|:|:|:|
Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

RESULT 14
AX498621
LOCUS AX498621 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 11 from Patent EP1229113.
ACCESSION AX498621
VERSION AX498621.1 GI:23343418
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 11 07-AUG-2002;
INVITROGEN CORPORATION (US)
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Best Local Similarity 88.0%; Pred. No. 19;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds  
(without alignments)  
782.095 Million cell updates/sec

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Perfect score: 25  
Sequence: 1 gttcagcttttctacwaagtgg 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: geneseqn2000s: \*  
4: geneseqn2001as: \*  
5: geneseqn2001bs: \*  
6: geneseqn2002as: \*  
7: geneseqn2002bs: \*  
8: geneseqn2003as: \*  
9: geneseqn2003bs: \*  
10: geneseqn2003cs: \*  
11: geneseqn2003ds: \*  
12: geneseqn2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.8	95.2	25	2	AAT48225 attP2, P3
2	23.8	95.2	25	2	AAT48224 attP1 cor
3	23.8	95.2	25	2	AAX78977 Oligonuc1
4	23.8	95.2	25	2	AAX78950 Oligonuc1
5	23.8	95.2	25	2	AAX78949 Oligonuc1
6	23.8	95.2	25	4	AAC87880 Escherich
7	23.8	95.2	25	4	AAC87876 Escherich
8	23.8	95.2	25	4	AAC87881 Escherich
9	23.8	95.2	25	4	AAT55749 Recombina
10	23.8	95.2	25	4	AAT55745 Recombina
11	23.8	95.2	25	4	AAT55750 Recombina
12	23.8	95.2	25	4	AAD14443 Recombina
13	23.8	95.2	25	4	AAD14444 Recombina
14	23.8	95.2	25	4	AAD14439 Recombina
15	23.8	95.2	25	5	AAS14786 Lambda ph
16	23.8	95.2	25	6	ABQ82128 Core sequ
17	23.8	95.2	25	6	ABQ82123 Core sequ
18	23.8	95.2	25	6	ABQ82127 Core sequ
19	23.8	95.2	25	8	ABT16635 Artificia
20	23.8	95.2	25	8	ABT16630 Artificia
21	23.8	95.2	25	8	ABT16634 Artificia

22	23.8	95.2	25	9	ACD28290	Nucleic a
23	23.8	95.2	25	9	ACD28286	Nucleic a
24	23.8	95.2	25	9	ACD28291	Nucleic a
25	23.8	95.2	25	9	ACD28490	Nucleic a
26	23.8	95.2	25	9	ACD28486	Nucleic a
27	23.8	95.2	25	9	ACD28491	Nucleic a
28	23.8	95.2	25	9	ADA38172	DNA of a
29	23.8	95.2	25	9	ADA38177	DNA of a
30	23.8	95.2	25	9	ADA38176	DNA of a
31	23.8	95.2	25	10	AAD60572	Core regi
32	23.8	95.2	25	10	AAD60573	Core regi
33	23.8	95.2	25	10	AAD60568	Core regi
34	23.8	95.2	25	10	ACC44664	Recombina
35	23.8	95.2	25	10	ACC44665	Recombina
36	23.8	95.2	25	10	ACC44660	Recombina
37	23.8	95.2	25	12	ADL93426	Recombina
38	23.8	95.2	25	12	ADL93430	Recombina
39	23.8	95.2	25	12	ADL93431	Recombina
40	23.8	95.2	27	4	AS06183	Phage-lam
41	23.8	95.2	27	4	AS06175	Phage-lam
42	23.8	95.2	27	4	AS06179	Phage-lam
43	23.8	95.2	27	4	AAF61424	AttP DNA
44	23.8	95.2	27	10	ABZ58736	Att site
45	23.8	95.2	27	10	ABZ58732	Att site

#### ALIGNMENTS

RESULT 1  
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ID AAT48225 standard; DNA; 25 BP.  
XX  
AC AAT48225;  
XX  
DT 20-OCT-1997 (first entry)  
XX  
DE attP2,P3 core region.  
XX  
KW att recombination site; core region; mutation; enhance; recombination;  
KW vector; subcloning; regulation; exchange; ss.  
XX  
OS Synthetic.  
XX  
PN WO9640724-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 07-JUN-1996; 96WO-US010082.  
XX  
PR 07-JUN-1995; 95US-00486139.  
XX  
(LIFE-) LIFE TECHNOLOGIES INC.  
XX  
PI Hartley JL, Brasch MA;  
XX  
DR WPI; 1997-065168/06.  
XX  
PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
PT using recombinant proteins and engineered recombination sites in vitro or  
PT in vivo.  
XX  
Claim 14; Page 56; 106pp; English.  
XX  
AAT48210-25 are att recombination site core region DNA sequences. The  
core region has at least one engineered mutation that enhances  
recombination in vitro in the formation of a Cointegrate or Product DNA.  
These core regions can be incorporated into novel vector donor DNA  
molecules. The nucleic acids, vectors and methods of the invention are  
used to obtain chimeric nucleic acid using recombination proteins and  
engineered recombination sites in vitro or in vivo. The improved  
specificity, speed and yields of the invention facilitates DNA or RNA  
subcloning, regulation or exchange useful for any related purpose, e.g.

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion  
CC or modification of transcribed, replicated, isolated or genomic DNA or  
CC RNA

Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

**Query Match** 95.2%; Score 23.8; DB 2; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.6;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25

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ID AAT48224 standard; DNA; 25 BP.

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AC AAT48224;

XX  
DT 20-OCT-1997 (first entry)

XX

DE attP1 core region.

att recombination site; core region; mutation; enhance; recombination;  
KW vector; subcloning; regulation; exchange; ss.

—

OS Synthetic.

XX

PN WO9640724-A1.

XX

PD 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010082.

XX  
PR 07-JUN-1995; 95US-00486139.

XX  
PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;

XX  
XX  
DR WPI: 1997-065168/06.

Nucleic acids, vectors and methods to obtain chimeric nucleic acid -  
PT using recombinant proteins and engineered recombination sites in vitro or  
PT in vivo.

Claim 14: Page 56; 106pp; English.

XX  
CC AAT48210-25 are att recombination site core region DNA sequences. The  
CC core region has at least one engineered mutation that enhances  
CC recombination *in vitro* in the formation of a Cointegrate or Product DNA.  
CC These core regions can be incorporated into novel vector donor DNA  
CC molecules. The nucleic acids, vectors and methods of the invention are  
CC used to obtain chimeric nucleic acid using recombination proteins and  
CC engineered recombination sites *in vitro* or *in vivo*. The improved  
CC specificity, speed and yields of the invention facilitates DNA or RNA  
CC subcloning, regulation or exchange useful for any related purpose, e.g.  
CC *in vitro* recombination of DNA segments, and *in vitro* or *in vivo* insertion  
CC or modification of transcribed, replicated, isolated or genomic DNA or  
CC RNA

Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 U; 0 Other;

Query Match 95.2%; Score 23.8; DB 2; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.6;

Matches	22;	Conservative	3;	Mismatches	0;	Indels	0;	Gaps	0
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QY 1 GTTCAGCTTTTTRTACWAAGTTGG 25

1 GTTCAGCTTTTTTGTACAAAGTTGG 25

OS Synthetic.  
 XX WO9921977-A1.  
 PN  
 XX  
 PD 06-MAY-1999.  
 XX  
 PF 26-OCT-1998; 98WO-US022589.  
 XX  
 PR 24-OCT-1997; 97US-0065930P.  
 PR 23-OCT-1998; 98US-00177387.  
 XX  
 PA (LIFE-) LIFE TECHNOLOGIES INC.  
 XX  
 PI Hartley JL, Brasch MA, Temple GF, Fox DK;  
 XX WPI; 1999-303011/25.  
 DR  
 XX  
 PT New nucleic acid cloning methods.  
 XX  
 PS Disclosure; Page 163; 185pp; English.  
 XX  
 CC The invention relates to novel methods for cloning or subcloning one or  
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
 CC more desired nucleic acid segments flanked by at least 2 recombination  
 CC sites which do not recombine with each other; (2) one or more vector  
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
 CC not recombine with each other; and (3) one or more site-specific  
 CC recombination proteins; (b) incubating the combination to transfer one or  
 CC more of the desired segments into one or more of the VDMs, thereby  
 CC producing one or more desired product molecules (PMs). The methods can be  
 CC used for the efficient and specific recombination of NAM segments. They  
 CC can be used to generate chimeric DNA or RNA molecules that have the  
 CC desired characteristics and/or nucleic acid segments. The methods can  
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
 CC are used in the method of the invention  
 XX  
 SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;  
 Query Match 95.2%; Score 23.8; DB 2; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 1.6;  
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25  
 Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
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 ID AAX78949 standard; DNA; 25 BP.  
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 AC AAX78949;  
 XX  
 DT 17-AUG-1999 (first entry)  
 XX  
 DE Oligonucleotide #15 for recombination and cloning method.  
 XX  
 KW Cloning; donor; recombination site; vector; chimeric; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9921977-A1.  
 XX  
 PD 06-MAY-1999.  
 XX  
 PF 26-OCT-1998; 98WO-US022589.  
 XX  
 PR 24-OCT-1997; 97US-0065930P.  
 PR 23-OCT-1998; 98US-00177387.  
 XX  
 PA (LIFE-) LIFE TECHNOLOGIES INC.  
 XX  
 PI Hartley JL, Brasch MA, Temple GF, Fox DK;  
 XX WPI; 1999-303011/25.  
 DR  
 XX  
 PT New nucleic acid cloning methods.  
 XX  
 PS Disclosure; Page 163; 185pp; English.  
 XX  
 CC The invention relates to novel methods for cloning or subcloning one or  
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
 CC more desired nucleic acid segments flanked by at least 2 recombination  
 CC sites which do not recombine with each other; (2) one or more vector  
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
 CC not recombine with each other; and (3) one or more site-specific  
 CC recombination proteins; (b) incubating the combination to transfer one or  
 CC more of the desired segments into one or more of the VDMs, thereby  
 CC producing one or more desired product molecules (PMs). The methods can be  
 CC used for the efficient and specific recombination of NAM segments. They  
 CC can be used to generate chimeric DNA or RNA molecules that have the  
 CC desired characteristics and/or nucleic acid segments. The methods can  
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
 CC are used in the method of the invention  
 XX  
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 Query Match 95.2%; Score 23.8; DB 2; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 1.6;  
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25  
 Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
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 ID AAX78949 standard; DNA; 25 BP.  
 XX  
 AC AAX78949;  
 XX  
 DT 17-AUG-1999 (first entry)  
 XX  
 DE Oligonucleotide #15 for recombination and cloning method.  
 XX  
 KW Cloning; donor; recombination site; vector; chimeric; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9921977-A1.  
 XX  
 PD 06-MAY-1999.  
 XX  
 PF 26-OCT-1998; 98WO-US022589.  
 XX  
 PR 24-OCT-1997; 97US-0065930P.  
 PR 23-OCT-1998; 98US-00177387.  
 XX  
 PA (LIFE-) LIFE TECHNOLOGIES INC.  
 XX

PI Hartley JL, Brasch MA, Temple GF, Fox DK;  
 XX WPI; 1999-303011/25.  
 XX  
 PT New nucleic acid cloning methods.  
 XX  
 PS Disclosure; Page 162; 185pp; English.  
 XX  
 CC The invention relates to novel methods for cloning or subcloning one or  
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or  
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or  
 CC more desired nucleic acid segments flanked by at least 2 recombination  
 CC sites which do not recombine with each other; (2) one or more vector  
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do  
 CC not recombine with each other; and (3) one or more site-specific  
 CC recombination proteins; (b) incubating the combination to transfer one or  
 CC more of the desired segments into one or more of the VDMs, thereby  
 CC producing one or more desired product molecules (PMs). The methods can be  
 CC used for the efficient and specific recombination of NAM segments. They  
 CC can be used to generate chimeric DNA or RNA molecules that have the  
 CC desired characteristics and/or nucleic acid segments. The methods can  
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994  
 CC are used in the method of the invention  
 XX  
 SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 U; 0 Other;  
 Query Match 95.2%; Score 23.8; DB 2; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 1.6;  
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
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 ID AAC87880 standard; DNA; 25 BP.  
 XX  
 AC AAC87880;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Escherichia coli core region recombinant site attP1 SEQ ID NO:15.  
 XX  
 KW Core region; recombination site; cloning; chimeric DNA; characteristic;  
 KW mutation; att site; lox site; ss.  
 XX  
 OS Escherichia coli.  
 XX  
 PN US61433557-A.  
 XX  
 PD 07-NOV-2000.  
 XX  
 PF 20-JAN-1999; 99US-00233493.  
 XX  
 PR 07-JUN-1995; 95US-00486139.  
 PR 07-JUN-1996; 96US-00663002.  
 PR 12-JAN-1998; 98US-00005476.  
 XX  
 PA (LIFE-) LIFE TECHNOLOGIES INC.  
 XX  
 PI Brasch MA, Hartley JL;  
 XX WPI; 2001-049004/06.  
 XX  
 DR Isolated nucleic acid molecules comprising a DNA segment having two  
 XX engineered recombination sites, derived from att or lox, which flank a  
 XX selectable marker and comprise a core region having an engineered  
 XX mutation.  
 XX  
 PS Claim 1; Col 18; 73pp; English.  
 XX

CC The present invention describes an isolated nucleic acid molecule (I)  
 CC comprising a first nucleic acid sequence having a defined sequence  
 CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,  
 CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described  
 CC are: (1) an isolated nucleic acid molecule (II) comprising a first  
 CC mutated recombination site that removes one or more stop codons from the  
 CC recombination site or avoids hairpin formation, the recombination site  
 CC being an att or lox site; (2) an isolated nucleic acid molecule (III)  
 CC comprising a first att recombination site comprising a mutation that  
 CC enhances recombination specificity; (3) vectors (IV) comprising the above  
 CC mentioned nucleic acids; and (4) cells comprising the above mentioned  
 CC nucleic acids or (IV). The nucleic acids are used in engineering a core  
 CC region of a given recombination site to provide mutative sites suitable  
 CC for subcloning reactions. The use of nucleic acids for obtaining  
 CC engineered recombination in vitro or in vivo makes the methods for DNA or  
 CC RNA subcloning, highly specific, rapid, and less labour intensive  
 XX

SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 U; 0 Other;  
 Query Match 95.2%; Score 23.8; DB 4; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 1.6;  
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACAAAGTTGG 25  
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 7  
 AAC87876  
 ID AAC87876 standard; DNA; 25 BP.  
 AC AAC87876;  
 XX  
 XX  
 DT 02-MAR-2001 (first entry)  
 DE Escherichia coli core region recombinant site attR3 SEQ ID NO:11.  
 XX  
 XX Core region; recombination site; cloning; chimeric DNA; characteristic;  
 KW mutation; att site; lox site; ss.  
 XX  
 XX Escherichia coli.  
 OS  
 XX US6143557-A.  
 PN 07-JUN-1995; 95US-00486139.  
 XX 07-JUN-1996; 96US-00663002.  
 XX 12-JAN-1998; 98US-00005476.  
 PD 07-NOV-2000.  
 XX  
 XX 20-JAN-1999; 99US-00233493.  
 PF  
 PR 07-JUN-1995; 95US-00486139.  
 PR 07-JUN-1996; 96US-00663002.  
 PR 12-JAN-1998; 98US-00005476.  
 XX  
 XX (LIFE-) LIFE TECHNOLOGIES INC.  
 PA  
 PI Brasch MA, Hartley JL;  
 XX  
 XX WPI; 2001-049004/06.  
 DR  
 XX Isolated nucleic acid molecules comprising a DNA segment having two  
 PT engineered recombination sites, derived from att or lox, which flank a  
 PT selectable marker and comprise a core region having an engineered  
 PT mutation.  
 XX  
 XX Claim 1; Col 18; 73pp; English.  
 PS  
 XX The present invention describes an isolated nucleic acid molecule (I)  
 CC comprising a first nucleic acid sequence having a defined sequence  
 CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,  
 CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described  
 CC are: (1) an isolated nucleic acid molecule (II) comprising a first  
 CC mutated recombination site that removes one or more stop codons from the  
 CC recombination site or avoids hairpin formation, the recombination site  
 CC being an att or lox site; (2) an isolated nucleic acid molecule (III)  
 CC comprising a first att recombination site comprising a mutation that  
 CC enhances recombination specificity; (3) vectors (IV) comprising the above  
 CC mentioned nucleic acids; and (4) cells comprising the above mentioned  
 CC nucleic acids or (IV). The nucleic acids are used in engineering a core  
 CC region of a given recombination site to provide mutative sites suitable  
 CC for subcloning reactions. The use of nucleic acids for obtaining  
 CC engineered recombination in vitro or in vivo makes the methods for DNA or  
 CC RNA subcloning, highly specific, rapid, and less labour intensive  
 XX

CC being an att or lox site; (2) an isolated nucleic acid molecule (III)  
 CC comprising a first att recombination site comprising a mutation that  
 CC enhances recombination specificity; (3) vectors (IV) comprising the above  
 CC mentioned nucleic acids; and (4) cells comprising the above mentioned  
 CC nucleic acids or (IV). The nucleic acids are used in engineering a core  
 CC region of a given recombination site to provide mutative sites suitable  
 CC for subcloning reactions. The use of nucleic acids for obtaining  
 CC engineered recombination in vitro or in vivo makes the methods for DNA or  
 CC RNA subcloning, highly specific, rapid, and less labour intensive  
 XX

SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;  
 Query Match 95.2%; Score 23.8; DB 4; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 1.6;  
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACAAAGTTGG 25  
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 8  
 AAC87881  
 ID AAC87881 standard; DNA; 25 BP.  
 AC AAC87881;  
 XX  
 XX  
 DT 02-MAR-2001 (first entry)  
 DE Escherichia coli core region recombinant site attP2,P3 SEQ ID NO:16.  
 XX  
 XX Core region; recombination site; cloning; chimeric DNA; characteristic;  
 KW mutation; att site; lox site; ss.  
 XX  
 XX Escherichia coli.  
 OS  
 XX US6143557-A.  
 PN 07-NOV-2000.  
 XX  
 XX 20-JAN-1999; 99US-00233493.  
 PF  
 PR 07-JUN-1995; 95US-00486139.  
 PR 07-JUN-1996; 96US-00663002.  
 PR 12-JAN-1998; 98US-00005476.  
 XX  
 XX (LIFE-) LIFE TECHNOLOGIES INC.  
 PA  
 PI Brasch MA, Hartley JL;  
 XX  
 XX WPI; 2001-049004/06.  
 DR  
 XX Isolated nucleic acid molecules comprising a DNA segment having two  
 PT engineered recombination sites, derived from att or lox, which flank a  
 PT selectable marker and comprise a core region having an engineered  
 PT mutation.  
 XX  
 XX Claim 1; Col 18; 73pp; English.  
 PS  
 XX The present invention describes an isolated nucleic acid molecule (I)  
 CC comprising a first nucleic acid sequence having a defined sequence  
 CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,  
 CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described  
 CC are: (1) an isolated nucleic acid molecule (II) comprising a first  
 CC mutated recombination site that removes one or more stop codons from the  
 CC recombination site or avoids hairpin formation, the recombination site  
 CC being an att or lox site; (2) an isolated nucleic acid molecule (III)  
 CC comprising a first att recombination site comprising a mutation that  
 CC enhances recombination specificity; (3) vectors (IV) comprising the above  
 CC mentioned nucleic acids; and (4) cells comprising the above mentioned  
 CC nucleic acids or (IV). The nucleic acids are used in engineering a core  
 CC region of a given recombination site to provide mutative sites suitable  
 CC for subcloning reactions. The use of nucleic acids for obtaining  
 CC engineered recombination in vitro or in vivo makes the methods for DNA or  
 CC RNA subcloning, highly specific, rapid, and less labour intensive  
 XX



XX OS Unidentified.

XX OS Unidentified.

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PN US6171861-B1.
XX
XX
PD 09-JAN-2001.
XX
XX 12-JAN-1998; 99US-00005476.
XX
XX 07-JUN-1995; 95US-00486139.
XX
XX 07-JUN-1996; 96US-00663002.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2001-136877/14.
XX
XX In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host.
XX
XX Claim 25; Col 46; 73pp; English.
XX
XX The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule, and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
XX invention
XX
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;
SQ
Query Match 95.2%; Score 23.8; DB 4; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.6;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTTRTACWAAGTTGG 25
DB 1 GTTCAGCTTTCTGTACAAAGTTGG 25
RESULT 12
AADI4443
ID AADI4443 standard; DNA; 25 BP.
XX
XX AADI4443;
XX
XX 01-NOV-2001 (first entry)
XX
XX Recombination site attP1 DNA.
XX
XX Recombination site; copy number; replicon; recombinatorial cloning;
XX attP1; ds.
XX
XX Unidentified.
XX
XX US6270969-B1.
XX
XX 07-AUG-2001.
XX
XX 20-JAN-1999; 99US-00233492.
XX
XX 07-JUN-1995; 95US-00486139.
XX
XX 07-JUN-1996; 96US-00663002.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2001-136877/14.
XX
XX Methods for apposing nucleic acids comprising an expression signal and a
PT gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under conditions
PT for recombination.
XX
XX Claim 14; Col 18; 76pp; English.
XX
XX The invention relates to a method for apposing an expression signal and a
CC gene or partial gene, using recombinatorial cloning. The method incubates
CC nucleic acids comprising the expression signal and the gene/ partial gene
CC in the presence of a recombination protein under conditions sufficient to
CC cause recombination and therefore appose the expression signal and the
CC gene or partial gene. The methods are useful for apposing an expression
CC signal and a gene or partial gene using recombinatorial cloning. The
CC methods are also useful for changing vectors, constructing genes for
CC fusion proteins, changing copy number, changing replicons, cloning into
CC phages, and cloning e.g., PCR products (with an attB site at one end and
CC a loxP site at the other end), genomic DNAs, and cDNAs. The methods are
CC highly specific, rapid, and less labour intensive than prior art methods.
CC The present sequence is a recombination site useful for recombination
XX cloning
XX
XX Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 U; 0 Other;
SQ
Query Match 95.2%; Score 23.8; DB 4; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.6;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTTRTACWAAGTTGG 25
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
RESULT 13
AADI4444
ID AADI4444 standard; DNA; 25 BP.
XX
XX AADI4444;
XX
XX 01-NOV-2001 (first entry)
XX
XX Recombination site attP2,P3 DNA.
XX
XX Recombination site; copy number; replicon; recombinatorial cloning;
XX attP2,P3; ds.
XX
XX Unidentified.
XX
XX US6270969-B1.
XX
XX 07-AUG-2001.
XX
XX 20-JAN-1999; 99US-00233492.
XX
XX 07-JUN-1995; 95US-00486139.
XX
XX 07-JUN-1996; 96US-00663002.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2001-488248/53.
XX
XX Methods for apposing nucleic acids comprising an expression signal and a
PT gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under conditions
PT for recombination.
XX
XX Claim 14; Col 18; 76pp; English.
XX
XX The invention relates to a method for apposing an expression signal and a
XX

```



SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 95.2%; Score 23.8; DB 5; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.6;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25

Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

Search completed: November 16, 2004, 04:02:50

Job time : 168.8 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds  
(without alignments)  
494.978 Million cell updates/sec

Title: US-10-820-133-43  
Perfect score: 25  
Sequence: 1 gttcagcttctttacwaagttgg 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.8	95.2	25	3	US-09-233-493-11
2	23.8	95.2	25	3	US-09-233-493-15
3	23.8	95.2	25	3	US-09-233-493-16
4	23.8	95.2	25	3	US-09-005-476-11
5	23.8	95.2	25	3	US-09-005-476-15
6	23.8	95.2	25	3	US-09-005-476-16
7	23.8	95.2	25	3	US-09-233-492-11
8	23.8	95.2	25	3	US-09-233-492-15
9	23.8	95.2	25	3	US-09-233-492-16
10	23.8	95.2	25	3	US-09-296-280-15
11	23.8	95.2	25	3	US-09-296-280-16
12	23.8	95.2	25	3	US-09-296-280-43
13	23.8	95.2	25	4	US-09-498-074-11
14	23.8	95.2	25	4	US-09-498-074-15
15	23.8	95.2	25	4	US-09-498-074-16
16	23.8	95.2	25	4	US-09-498-074-11
17	23.8	95.2	25	4	US-09-498-074-15
18	23.8	95.2	25	4	US-09-498-074-16
19	23.8	95.2	25	5	PCT-US96-10082A-11
20	23.8	95.2	25	5	PCT-US96-10082A-15
21	23.8	95.2	25	5	PCT-US96-10082A-16
22	23.8	95.2	201	1	US-08-021-667A-18
23	23.8	95.2	201	1	US-08-410-544-18
24	23.8	95.2	201	1	US-08-728-785A-18
25	23.8	95.2	1763	4	US-09-244-805-57
26	23.8	95.2	4909	3	US-08-556-978B-78
27	23.8	95.2	6043	4	US-09-630-929-4

28 23.8 95.2 7652 1 US-07-590-988A-1 Sequence 1, Appli  
29 22 88.0 25 3 US-09-236-280-42 Sequence 42, Appl  
30 21.2 84.8 25 3 US-09-233-493-9 Sequence 9, Appli  
31 21.2 84.8 25 3 US-09-233-493-10 Sequence 10, Appl  
32 21.2 84.8 25 3 US-09-005-476-9 Sequence 9, Appli  
33 21.2 84.8 25 3 US-09-005-476-10 Sequence 10, Appl  
34 21.2 84.8 25 3 US-09-233-492-9 Sequence 9, Appli  
35 21.2 84.8 25 3 US-09-233-492-10 Sequence 10, Appl  
36 21.2 84.8 25 3 US-09-296-280-9 Sequence 9, Appli  
37 21.2 84.8 25 3 US-09-296-280-10 Sequence 10, Appl  
38 21.2 84.8 25 3 US-09-296-280-11 Sequence 11, Appl  
39 21.2 84.8 25 4 US-09-498-074-9 Sequence 9, Appli  
40 21.2 84.8 25 4 US-09-498-074-10 Sequence 10, Appl  
41 21.2 84.8 25 4 US-09-498-074-9 Sequence 9, Appli  
42 21.2 84.8 25 4 US-09-498-074-10 Sequence 10, Appl  
43 21.2 84.8 25 5 PCT-US96-10082A-9 Sequence 9, Appli  
44 21.2 84.8 25 5 PCT-US96-10082A-10 Sequence 10, Appl  
45 20.8 83.2 25 3 US-09-233-493-14 Sequence 14, Appl

## ALIGNMENTS

RESULT 1  
US-09-233-493-11  
; Sequence 11, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
US-09-233-493-11

Query Match 95.2%; Score 23.8; DB 3; Length 25;  
Best Local Similarity 88.0%; Pred. No. 0.29;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25  
|||||:|||||:|||||:|||||  
Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

## RESULT 2

US-09-233-493-15  
; Sequence 15, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2540  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
US-09-233-493-15

Query Match 95.2%; Score 23.8; DB 3; Length 25;  
Best Local Similarity 88.0%; Pred. No. 0.29;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25  
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Db 1 GTTCAGCTTTTGTCACAAAGTTGG 25

## RESULT 3

US-09-233-493-16  
; Sequence 16, Application US/09233493  
; Patent No. 6143557  
; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2540  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
US-09-233-493-16

Query Match 95.2%; Score 23.8; DB 3; Length 25;  
Best Local Similarity 88.0%; Pred. No. 0.29;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25  
|||||:|||||:|||||:|||||  
Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

## RESULT 4

US-09-005-476-11  
; Sequence 11, Application US/09005476  
; Patent No. 6171861  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

Query Match 95.2%; Score 23.8; DB 3; Length 25;

RESULT 7  
US-09-233-492-11  
; Sequence 11, Application US/09233492  
; Patent No. 6270969  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600

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/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/233,492
/ FILING DATE: 20-JAN-1999
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ US-09-233-492-11

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.29;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAAGTTGG 25
Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 8
US-09-233-492-15
/ Sequence 15, Application US/09233492
/ Patent No. 6270969
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/233,492
/ FILING DATE: 20-JAN-1999
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ US-09-233-492-16

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.29;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 9
US-09-233-492-16
/ Sequence 16, Application US/09233492
/ Patent No. 6270969
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/233,492
/ FILING DATE: 20-JAN-1999
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
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/ FILING DATE: 07-JUN-1995
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/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ US-09-233-492-16

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.29;
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Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 9
US-09-233-492-16
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/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
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/ CITY: Washington
/ STATE: DC
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/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
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/ TELEFAX: 202-371-2540
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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
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/ US-09-233-492-16

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; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/296,280
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
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; OTHER INFORMATION: Description of Unknown Organism: recombination
; US-09-296-280-15

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; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/296,280
; EARLIER FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
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; TYPE: DNA
; ORGANISM: Unknown
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; US-09-296-280-16

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; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
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; US-09-296-280-43

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; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
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; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
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RESULT 12
US-09-296-280-43
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; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
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; EARLIER FILING DATE: 1997-10-24
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RESULT 13
US-09-498-074-11
; Sequence 11, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
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; APPLICATION NUMBER: 09/005,476
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; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
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; LENGTH: 25 base pairs
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; STRANDEDNESS: both
; TOPOLOGY: both
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; Sequence 15, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
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; FILING DATE: 07-JUN-1995
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; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
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; COMPUTER: IBM PC compatible
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; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
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; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
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; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
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; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
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; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
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; FILING DATE: 07-JUN-1996
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-10-820-133-43

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	23.8	95.2	25	9	US-09-907-900-15
6	23.8	95.2	25	9	US-09-907-900-16
7	23.8	95.2	25	9	US-09-907-900-43
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9	23.8	95.2	25	9	US-09-907-719-16
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11	23.8	95.2	25	10	US-09-432-085-11
12	23.8	95.2	25	10	US-09-432-085-15

13	23.8	95.2	25	10	US-09-432-085-16	Sequence 16, Appl
14	23.8	95.2	25	10	US-09-985-448-15	Sequence 15, Appl
15	23.8	95.2	25	10	US-09-985-448-16	Sequence 16, Appl
16	23.8	95.2	25	10	US-09-985-448-43	Sequence 43, Appl
17	23.8	95.2	25	14	US-10-055-001A-6	Sequence 6, Appl
18	23.8	95.2	25	14	US-10-055-001A-10	Sequence 10, Appl
19	23.8	95.2	25	14	US-10-055-001A-11	Sequence 11, Appl
20	23.8	95.2	25	14	US-10-058-292-11	Sequence 11, Appl
21	23.8	95.2	25	14	US-10-058-292-15	Sequence 15, Appl
22	23.8	95.2	25	14	US-10-058-292-16	Sequence 16, Appl
23	23.8	95.2	25	14	US-10-058-291-11	Sequence 11, Appl
24	23.8	95.2	25	14	US-10-058-291-15	Sequence 15, Appl
25	23.8	95.2	25	14	US-10-058-291-16	Sequence 16, Appl
26	23.8	95.2	25	14	US-10-162-879-11	Sequence 11, Appl
27	23.8	95.2	25	14	US-10-162-879-15	Sequence 15, Appl
28	23.8	95.2	25	14	US-10-162-879-16	Sequence 16, Appl
29	23.8	95.2	25	15	US-10-161-403-51	Sequence 51, Appl
30	23.8	95.2	25	15	US-10-161-403-55	Sequence 55, Appl
31	23.8	95.2	25	15	US-10-161-403-56	Sequence 56, Appl
32	23.8	95.2	25	15	US-10-300-892-15	Sequence 15, Appl
33	23.8	95.2	25	15	US-10-300-892-16	Sequence 16, Appl
34	23.8	95.2	25	15	US-10-300-892-43	Sequence 43, Appl
35	23.8	95.2	25	16	US-10-680-316-15	Sequence 15, Appl
36	23.8	95.2	25	16	US-10-680-316-16	Sequence 16, Appl
37	23.8	95.2	25	16	US-10-680-316-43	Sequence 43, Appl
38	23.8	95.2	25	17	US-10-815-730-15	Sequence 15, Appl
39	23.8	95.2	25	17	US-10-815-730-16	Sequence 16, Appl
40	23.8	95.2	25	17	US-10-815-730-43	Sequence 43, Appl
41	23.8	95.2	25	17	US-10-820-133-15	Sequence 15, Appl
42	23.8	95.2	25	17	US-10-820-133-16	Sequence 16, Appl
43	23.8	95.2	25	17	US-10-820-133-43	Sequence 43, Appl
44	23.8	95.2	25	18	US-10-161-408-42	Sequence 42, Appl
45	23.8	95.2	25	18	US-10-161-408-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-09-855-797A-15

; Sequence 15, Application US/09855797A

; Patent No. US20020094574A1

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.

; APPLICANT: Fox, Donna K.

; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

; TITLE OF INVENTION: Recombination Sites

; FILE REFERENCE: 0942.2850008

; CURRENT APPLICATION NUMBER: US/09/855.797A

; PRIOR FILING DATE: 2001-05-16

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: US 60/065,930

; PRIOR FILING DATE: 1997-10-24

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: recombination

; OTHER INFORMATION: products

US-09-855-797A-15

Query Match 95.2%; Score 23.8; DB 9; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.1;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTCACWAAAGTTGG 25

|||||:|||||:|||||:|||||

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

## RESULT 2

US-09-855-797A-16  
; Sequence 16, Application US/09855797A  
; Patent No. US20020094574A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850008  
; CURRENT APPLICATION NUMBER: US/09/855,797A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/296,281  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-855-797A-16

Query Match 95.2%; Score 23.8; DB 9; Length 25;  
Best Local Similarity 88.0%; Pred. No. 1.1;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

## RESULT 3

US-09-855-797A-43  
; Sequence 43, Application US/09855797A  
; Patent No. US20020094574A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850008  
; CURRENT APPLICATION NUMBER: US/09/855,797A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/296,281  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/065,930  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-855-797A-43

Query Match 95.2%; Score 23.8; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

## RESULT 4

US-09-822-634-8  
; Sequence 8, Application US/09822634  
; Patent No. US20020150556A1  
; GENERAL INFORMATION:  
; APPLICANT: Vile, Richard G.  
; APPLICANT: Harrington, Kevin  
; APPLICANT: Bateman, Andrew  
; APPLICANT: Murphy, Steven  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE  
; FILE REFERENCE: 07039-289001  
; CURRENT APPLICATION NUMBER: US/09/822,634  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/193,977  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated vector sequence  
US-09-822-634-8

Query Match 95.2%; Score 23.8; DB 9; Length 25;  
Best Local Similarity 88.0%; Pred. No. 1.1;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

## RESULT 5

US-09-907-900-15  
; Sequence 15, Application US/09907900  
; Patent No. US20020172997A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,900  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-900-15

Query Match 95.2%; Score 23.8; DB 9; Length 25;  
Best Local Similarity 88.0%; Pred. No. 1.1;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
|||||

RESULT 6  
US-09-907-900-16  
; Sequence 16, Application US/09907900  
; Patent No. US20020172997A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,900  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-900-16

Query Match 95.2%; Score 23.8; DB 9; Length 25;  
Best Local Similarity 88.0%; Pred. No. 1.1;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
|||||

Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
|||||

RESULT 7  
US-09-907-900-43  
; Sequence 43, Application US/09907900  
; Patent No. US20020172997A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,900  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-900-43

Query Match 95.2%; Score 23.8; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
|||||

Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
|||||

RESULT 8  
US-09-907-719-15  
; Sequence 15, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-719-15

Query Match 95.2%; Score 23.8; DB 9; Length 25;  
Best Local Similarity 88.0%; Pred. No. 1.1;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
|||||

Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
|||||

RESULT 9  
US-09-907-719-16  
; Sequence 16, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; TITLE OF INVENTION: Recombination Sites  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-719-16

Query Match 95.2%; Score 23.8; DB 9; Length 25;  
Best Local Similarity 88.0%; Pred. No. 1.1;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
|||||

Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25  
|||||

## RESULT 10

US-09-907-719-43  
; Sequence 43, Application US/09907719  
; Publication No. US20020192819A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; APPLICANT: Temple, Gary F.  
; APPLICANT: Fox, Donna K.  
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having  
; FILE REFERENCE: 0942.2850004  
; CURRENT APPLICATION NUMBER: US/09/907,719  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/177,387  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: recombination  
; OTHER INFORMATION: products  
US-09-907-719-43

Query Match 95.2%; Score 23.8; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25  
|||||:|||||:|||||:|||||  
Db 1 GTTCAGCTTTTTRTACWAAGTTGG 25

## RESULT 11

US-09-432-085-11  
; Sequence 11, Application US/09432085  
; Publication No. US20030100110A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,085  
; FILING DATE: (Herewith)  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: 08/486,139  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
US-09-432-085-11

Query Match 95.2%; Score 23.8; DB 10; Length 25;  
Best Local Similarity 88.0%; Pred. No. 1.1;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25  
|||||:|||||:|||||:|||||  
Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

## RESULT 12

US-09-432-085-15  
; Sequence 15, Application US/09432085  
; Publication No. US20030100110A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; APPLICANT: Brasch, Michael A.  
; TITLE OF INVENTION: Recombinational Cloning Using Engineered  
; TITLE OF INVENTION: Recombination Sites  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 New York Ave., N. W. Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,085  
; FILING DATE: (Herewith)  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/233,493  
; FILING DATE: 20-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,476  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/663,002  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/486,139  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540



INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cdna

US-09-432-085-15

Query Match 95.2%; Score 23.8; DB 10; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.1;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACAAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 13

US-09-432-085-16

Sequence 16, Application US/09432085

Publication No. US20030100110A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered

TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C

STREET: 1100 New York Ave., N. W. Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/432,085

FILING DATE: (Herewith)

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/233,493

FILING DATE: 20-JAN-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,476

FILING DATE: 12-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/663,002

FILING DATE: 07-JUN-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486,139

FILING DATE: 07-JUN-1995

CLASSIFICATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cdna

US-09-432-085-16

Query Match 95.2%; Score 23.8; DB 10; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.1;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACAAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 14

US-09-985-448-15

Sequence 15, Application US/09985448

Publication No. US20030157716A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Fox, Donna K.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2850004

CURRENT APPLICATION NUMBER: US/09/985,448

CURRENT FILING DATE: 2001-11-02

PRIOR APPLICATION NUMBER: US/09/177,387

PRIOR FILING DATE: 1998-10-23

PRIOR APPLICATION NUMBER: US 60/065,930

PRIOR FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 15

LENGTH: 25

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: recombination

US-09-985-448-15

Query Match 95.2%; Score 23.8; DB 10; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.1;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACAAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 15

US-09-985-448-16

Sequence 16, Application US/09985448

Publication No. US20030157716A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Fox, Donna K.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2850004

CURRENT APPLICATION NUMBER: US/09/985,448

CURRENT FILING DATE: 2001-11-02

PRIOR APPLICATION NUMBER: US/09/177,387

PRIOR FILING DATE: 1998-10-23

PRIOR APPLICATION NUMBER: US 60/065,930

PRIOR FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 25

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: recombination

US-09-985-448-16

US-09-985-448-16

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 Best Local Similarity 88.0%; Pred. No. 1.1;  
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 Db 1 GTTCAGCTTTCTGTACAAAGTTGG 25

Search completed: November 16, 2004, 11:15:01  
 Job time : 314.1 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds  
(without alignments)  
594.643 Million cell updates/sec

Title: US-10-820-133-43  
Perfect score: 25  
Sequence: 1 gttcagctttttttacwaagttgg 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gse1:\*  
9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	23.8	95.2	206	5	BQ156416
C 2	23.8	95.2	299	5	BY115594
C 3	23.8	95.2	306	5	BP757615
C 4	23.8	95.2	374	5	BP754432
C 5	23.8	95.2	401	5	BP754410
C 6	23.8	95.2	409	5	BP754552
C 7	23.8	95.2	422	5	BP754464
C 8	23.8	95.2	423	5	BP754551
C 9	23.8	95.2	430	5	BP754589
C 10	23.8	95.2	432	5	BP754563
C 11	23.8	95.2	443	5	BP754508
C 12	23.8	95.2	443	5	BP754571
C 13	23.8	95.2	449	5	BP754440
C 14	23.8	95.2	472	5	BQ157398
C 15	23.8	95.2	473	5	BQ156404
C 16	23.8	95.2	482	5	BP754592
C 17	23.8	95.2	483	5	BP757892
C 18	23.8	95.2	486	5	BP754503
C 19	23.8	95.2	489	5	BP754581
C 20	23.8	95.2	546	5	BP754439
C 21	23.8	95.2	567	5	BP754491
C 22	23.8	95.2	597	4	BI422679
C 23	23.8	95.2	645	5	BP754484
C 24	23.8	95.2	671	5	BP754388

C 25	23.8	95.2	672	5	BP754535
C 26	23.8	95.2	674	5	BP754519
C 27	23.8	95.2	689	5	BP754572
C 28	23.8	95.2	695	8	AQ991039
C 29	23.8	95.2	712	8	AQ990809
C 30	23.8	95.2	731	5	BP758121
C 31	23.8	95.2	743	8	AQ990346
C 32	23.8	95.2	764	8	AQ990110
C 33	23.8	95.2	769	8	AQ990470
C 34	22.8	91.2	395	8	AQ991303
C 35	22.8	91.2	664	8	AQ991011
C 36	22.8	91.2	751	8	AQ989566
C 37	21.2	84.8	672	8	AQ990864
C 38	21.2	84.8	753	8	AQ990861
C 39	21.2	84.8	770	8	AQ991774
C 40	21.2	84.8	791	8	AQ991791
C 41	21.2	84.8	808	8	AQ990388
C 42	21.2	84.8	821	9	CL672759
C 43	21.2	84.8	875	9	CL688994
C 44	20.8	83.2	87	6	CB400039
C 45	20.8	83.2	90	6	CB392047

#### ALIGNMENTS

RESULT 1  
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LOCUS BQ156416 206 bp mRNA linear EST 24-APR-2002  
DEFINITION NF092F02IR1F1027 Irradiated Medicago truncatula cDNA clone  
ACCSSION BQ156416  
VERSION BQ156416.1 GI:20293475  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
REFERENCE 1 (bases 1 to 206)  
Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.,  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula irradiated library  
Unpublished (2001)  
JOURNAL  
COMMENT Contact: May GD  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 224 6650  
Fax: 580 224 6692  
Email: gdmay@noble.org  
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/note="Vector: Lambda Zap; Seedlings were exposed either  
to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.  
Gamma-irradiated samples were harvested at 6, 12, 24 and  
48 hours after treatment. UV-irradiated samples were  
harvested 24 hours post-treatment. cDNA was prepared from  
polyA+ enriched, pooled samples of equivalent amounts of  
total RNA from each sample. The cDNA was directionally  
ligated into the Uni-Zap XR vector (Stratagene) and

packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using EXAssistant helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

## ORIGIN

Query Match 95.2%; Score 23.8; DB 5; Length 206;  
Best Local Similarity 88.0%; Pred. No. 13;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25

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## RESULT 2

BY115594

LOCUS BY115594 RIKEN full-length enriched, 18 days embryo whole body Mus  
DEFINITION musculus cDNA clone L430040C03 5', mRNA sequence.

ACCESSION BY115594

VERSION BY115594.1 GI:26226695

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

## REFERENCE

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,  
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Mateuda, H.,  
Bacalov, S., Beisel, K. W., Blake, J. A., Bratt, D., Brusci, V.,  
Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,  
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,  
Gariboldi, M., Giesi, C., Godzik, A., Gough, J., Grimmond, S.,  
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,  
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongaya, A.,  
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,  
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
Numata, K., Okido, T., Pavan, W. J., Perlea, G., Pesole, G.,  
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,  
Ravasi, T., Read, J. C., Read, D. J., Reid, J., Ring, B. Z., Ringwald, M.,  
Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,  
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,  
Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,  
Rogers, J., Birney, E. and Hayaishizaki, Y.

Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

## COMMENT

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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
Hayaishizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

## FEATURES

source

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Db 246 GTTCAGCTTTTATACTAAGTTGG 270

## RESULT 3

LOCUS BP757615/c BP757615 306 bp mRNA linear EST 08-JUL-2004  
DEFINITION BP757615 mouse (C57BL/6) pancreatic islet library with  
recombination-based method Mus musculus cDNA clone mib04031 3',  
mRNA sequence.

ACCESSION BP757615

VERSION BP757615.1 GI:50077505

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 306)

AUTHORS Nishimura, M., Yokoi, N., Miki, T., Horikawa, Y., Yoshioka, H.,

Takeda, J., Ohara, O. and Seino, S.  
Construction of a multi-functional cDNA library specific for mouse  
pancreatic islets and its application to microarray

Unpublished (2004)

CONTACT: Susumu Seino

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Fax: 81-78-382-5370

Email: seino@med.kobe-u.ac.jp.

Location/Qualifiers

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Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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LOCUS BP754432 374 bp mRNA linear EST 08-JUL-2004
DEFINITION BP754432 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial0061 3',
mRNA sequence.
ACCESSION BP754432
VERSION BP754432.1 GI:50074322
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 374)
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
Unpublished (2004)
JOURNAL
COMMENT
Contact: Susumu Seino
Kobe University Graduate School of Medicine
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Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
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Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION BP754410 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial0045 3',
mRNA sequence.
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VERSION BP754410.1 GI:50074300
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 401)
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
Unpublished (2004)
JOURNAL
COMMENT
Contact: Susumu Seino
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
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DEFINITION BP754552 mouse (C57BL/6) pancreatic islet library with
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mRNA sequence.
ACCESSION BP754552
VERSION BP754552.1 GI:50074442
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 409)
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
Unpublished (2004)
JOURNAL
COMMENT
Contact: Susumu Seino
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1..409
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.

## REFERENCE

## AUTHORS

1 (bases 1 to 473)  
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

## TITLE

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

## JOURNAL

## COMMENT

Medicago truncatula irradiated library  
Unpublished (2001)

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 224 6650

Fax: 580 224 6692

Email: gdmay@noble.org

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## FEATURES

## source

Location/Qualifiers

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to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.  
Gamma-irradiated samples were harvested at 6, 12, 24 and  
48 hours after treatment. UV-irradiated samples were  
harvested 24 hours post-treatment. cDNA was prepared from  
polyA+ enriched, pooled samples of equivalent amounts of  
total RNA from each sample. The cDNA was directionally  
ligated into the Uni-Zap XR vector (Stratagene) and  
packaged using the Gigapack III Gold packaging extracts.  
Phagemids containing cDNA inserts were in vivo excised  
from the recombinant Uni-Zap XR vector using ExAssist  
helper phage and the E. coli strain XL1-Blue MRF'  
(Stratagene). Excised plasmids were plated using SOLR  
cells."

## ORIGIN

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Best Local Similarity 88.0%; Pred. NO.15;

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Job time : 1533 secs

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